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Query Match      82.7%; Score 347.5; DB 6; Length 206;
Best Local Similarity 82.9%; Pred. No. 1.5e-33;
Matches 63; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 2 NNYKIKCLGGVHTACKYG-SLKPNCGNKVVVSYGLTKQEKQDILKEHNDPQKRIARGLE 60
DB 3 NNYKIKCLGGVHTACKYG-SLKPNCGNKVVVSYGLTKQEKQDILKEHNDPQKRIARGLE 62
QY 61 TRGNPGQPQPAKMNKN 76
DB 63 TRGNPGQPQPAKMNKN 78

RESULT 3
US-10-533-811-1
; Sequence 1, Application US/10533811
; Publication No. US20060051364A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Barral, Aldina
; APPLICANT: Netto, Manoel
; APPLICANT: Brodekyn, Claudia
; APPLICANT: Gomes, Regis
; TITLE OF INVENTION: LU LONGIPALPIS POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 4239-67028-08
; CURRENT APPLICATION NUMBER: US/10/533,811
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/422,303
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/US2003/034453
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Lutzomyia longipalpis
US-10-533-811-1

Query Match      21.9%; Score 92; DB 6; Length 271;
Best Local Similarity 35.9%; Pred. No. 0.0029;
Matches 28; Conservative 11; Mismatches 27; Indels 12; Gaps 6;

QY 1 NNYKIK-CLKGGV---HTACK-YGSLKPNCGNKVVVSYGLTKQEKQDILKEHNDPQK 54
DB 21 SNYKQESCSGGVERPHIGCKNSGDFSETCGDAEIVK--MDKKQNLLVMHNRDR 78
QY 55 IARLETRGNPGQPQPAK 72
DB 79 FARG-----AVPGAPAAK 92

RESULT 4
US-10-527-500-23
; Sequence 23, Application US/10527500
; Publication No. US20060004186A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Fischer, Laurent Bernard
; APPLICANT: Audonnet, Jean-Cristophe
; APPLICANT: Milward, Francis William
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/412,327
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Phlebotomus perniciosus
US-10-527-500-23

Query Match      17.7%; Score 74.5; DB 6; Length 236;
Best Local Similarity 34.3%; Pred. No. 0.28;
Matches 23; Conservative 7; Mismatches 24; Indels 13; Gaps 4;

QY 1 NNYKIK-CLKGGV---HTACKYG-----SLKPNCGNKVVVSYGLTKQEKQDILKEHNDP 51
DB 20 NDYCPKLTGKTGKPHIGCRNNGDFDRSACPNDQAQV-----EMTQQRKELFLKIHRL 75
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; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/412,327
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Phlebotomus ariasi
US-10-527-500-23

Query Match      18.2%; Score 76.5; DB 6; Length 277;
Best Local Similarity 31.9%; Pred. No. 0.2;
Matches 22; Conservative 7; Mismatches 25; Indels 15; Gaps 3;

QY 1 NNYKIKCLKGG-----VHTACKYGSLS-----KPNCGNKVVVSYGLTKQEKQDILKEHN 49
DB 20 NDYCPKLTGKFNQVKTGKNDGKFVSTCPKNDQAQMI-----DMTEQRKELFLKIHRL 75
QY 50 DFRQKIARG 58
DB 76 RLDRRLARG 84

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US-10-527-500-65
; Sequence 65, Application US/10527500
; Publication No. US20060004186A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Fischer, Laurent Bernard
; APPLICANT: Audonnet, Jean-Cristophe
; APPLICANT: Milward, Francis William
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/412,327
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Phlebotomus perniciosus
US-10-527-500-65

Query Match      17.7%; Score 74.5; DB 6; Length 236;
Best Local Similarity 34.3%; Pred. No. 0.28;
Matches 23; Conservative 7; Mismatches 24; Indels 13; Gaps 4;

QY 1 NNYKIK-CLKGGV---HTACKYG-----SLKPNCGNKVVVSYGLTKQEKQDILKEHNDP 51
DB 20 NDYCPKLTGKTGKPHIGCRNNGDFDRSACPNDQAQV-----EMTQQRKELFLKIHRL 75
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 18.855 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLGGVHTACKY.....RGLTRNGPQPAPKMN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
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1	420	100.0	227	6	US-10-498-026-76	Sequence 76, Appl
2	347.5	82.7	206	6	US-10-498-026-80	Sequence 80, Appl
3	92	21.9	271	6	US-10-533-811-1	Sequence 1, Appl
4	76.5	18.2	277	6	US-10-527-500-23	Sequence 23, Appl
5	74.5	17.7	236	6	US-10-527-500-65	Sequence 65, Appl
6	70	16.7	253	7	US-11-153-222A-2	Sequence 2, Appl
7	70	16.7	298	7	US-11-124-367A-416	Sequence 416, Appl
8	70	16.7	298	7	US-11-124-367A-417	Sequence 417, Appl
9	70	16.7	298	7	US-11-124-367A-419	Sequence 419, Appl
10	70	16.7	313	7	US-11-124-367A-418	Sequence 418, Appl
11	70	16.7	416	7	US-11-124-367A-415	Sequence 415, Appl
12	66.5	15.8	377	7	US-11-096-568A-2865	Sequence 2865, Ap
13	66.5	15.8	377	7	US-11-096-568A-2867	Sequence 2867, Ap
14	66.5	15.8	409	7	US-11-079-463-6373	Sequence 6373, Ap
15	66.5	15.8	500	7	US-11-096-568A-2864	Sequence 2864, Ap
16	65.5	15.6	2871	7	US-11-169-041-131	Sequence 131, App
17	65.5	15.6	3002	6	US-10-821-234-916	Sequence 916, App
18	65	15.5	737	7	US-11-152-366-28	Sequence 28, Appl
19	64	15.2	135	7	US-11-188-298-3692	Sequence 3692, A
20	63	15.0	102	7	US-11-188-298-3770	Sequence 3770, Ap
21	62.5	14.9	332	7	US-11-188-298-3770	Sequence 3770, Ap
22	62.5	14.9	385	7	US-11-087-099-2354	Sequence 2354, Ap
23	62	14.8	254	7	US-11-172-740-2285	Sequence 2285, A
24	62	14.8	254	7	US-11-188-298-19953	Sequence 19953, A
25	62	14.8	423	7	US-11-087-099-5878	Sequence 5878, Ap

26	61	14.5	497	7	US-11-197-133A-16	Sequence 16, Appl
27	60	14.3	220	7	US-11-153-222A-3	Sequence 3, Appl
28	59.5	14.2	201	6	US-10-467-657-5346	Sequence 5346, Ap
29	59.5	14.2	378	7	US-11-129-143-49	Sequence 49, Appl
30	59	14.0	253	7	US-11-172-740-561	Sequence 561, Appl
31	58.5	13.9	838	7	US-11-031-737A-11	Sequence 11, Appl
32	58.5	13.9	838	7	US-11-031-482-11	Sequence 11, Appl
33	58	13.8	1560	6	US-10-204-639-63	Sequence 63, Appl
34	58	13.8	2911	7	US-11-090-817-706	Sequence 706, Appl
35	57.5	13.7	176	7	US-11-096-568A-1297	Sequence 1297, Ap
36	57.5	13.7	202	7	US-11-096-568A-1296	Sequence 1296, Ap
37	57.5	13.7	206	6	US-10-467-657-7716	Sequence 7716, Ap
38	57.5	13.7	443	7	US-11-172-740-528	Sequence 528, App
39	57.5	13.7	519	7	US-11-033-039-442	Sequence 442, App
40	57	13.6	231	6	US-10-821-234-943	Sequence 943, App
41	56.5	13.5	249	7	US-11-096-568A-33644	Sequence 33644, A
42	56.5	13.5	283	7	US-11-096-568A-33643	Sequence 33643, A
43	56.5	13.5	287	7	US-11-096-568A-33642	Sequence 33642, A
44	56.5	13.5	359	7	US-11-108-528-62	Sequence 62, Appl
45	56.5	13.5	453	7	US-11-096-568A-6095	Sequence 6095, Ap

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76

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Best Local Similarity 100.0%; Pred. No. 4.7e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	24	NNYCKIKLGGVHTACKYGLKPCNCGKVVSYGLTKQEKQDILKEHNDPROKIARGL	83
Qy	61	TRGNPGPQPAPKMNKN 76	
Db	84	TRGNPGPQPAPKMNKN 99	

RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80

QY 1 NNYCKIKLKGVTACKYGLKPKNCNKKVSVYGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGVTACKYGLKPKNCNKKVSVYGLTKQEKQDILKEHNDFRQKIARGLE 60
QY 61 TRGNPGQPAPKMKN 76
DB 61 TRGNPGQPAPKMKN 76

RESULT 2
US-08-614-935-2
; Sequence 2, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
US-08-614-935-2

Query Match 100.0%; Score 420; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNYCKIKLKGVTACKYGLKPKNCNKKVSVYGLTKQEKQDILKEHNDFRQKIARGLE 60
QY 61 TRGNPGQPAPKMKN 76
DB 61 TRGNPGQPAPKMKN 76

RESULT 3
US-09-130-287-2
; Sequence 2, Application US/09130287

; Patent No. 6106844
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,287
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
US-09-130-287-2

Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNYCKIKLKGVTACKYGLKPKNCNKKVSVYGLTKQEKQDILKEHNDFRQKIARGLE 60
QY 61 TRGNPGQPAPKMKN 76
DB 61 TRGNPGQPAPKMKN 76

RESULT 4
US-09-541-759-6
; Sequence 6, Application US/09541759
; Patent No. 6723322
; GENERAL INFORMATION:
; APPLICANT: Lustigman, Sara
; APPLICANT: Pearlman, Eric
; APPLICANT: Unnasch, Thomas
; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
; FILE REFERENCE: 63475/252
; CURRENT APPLICATION NUMBER: US/09/541,759
; CURRENT FILING DATE: 2000-04-03

Wed Apr 19 09:10:02 2006

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 22.916 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-95
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	420	100.0	204	1	US-08-614-935-2 Sequence 2, Appli
3	420	100.0	204	2	US-09-130-287-2 Sequence 2, Appli
4	420	100.0	227	1	US-09-541-759-6 Sequence 6, Appli
5	414	98.6	204	1	US-08-614-935-1 Sequence 1, Appli
6	414	98.6	204	2	US-09-130-287-1 Sequence 5, Appli
7	305	72.6	204	1	US-08-614-935-5 Sequence 5, Appli
8	305	72.6	204	2	US-09-130-287-5 Sequence 8, Appli
9	296.5	70.6	203	1	US-08-419-414-8 Sequence 3, Appli
10	296.5	70.6	203	1	US-08-614-935-3 Sequence 3, Appli
11	296.5	70.6	203	2	US-09-130-287-3 Sequence 4, Appli
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14	243	57.9	205	1	US-08-419-414-10 Sequence 6, Appli
15	243	57.9	205	1	US-08-614-935-6 Sequence 7, Appli
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19	180	42.9	31	1	US-08-614-935-46 Sequence 46, Appli
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22	174	41.4	31	2	US-09-130-287-45 Sequence 45, Appli
23	168	40.0	31	1	US-08-614-935-53 Sequence 53, Appli
24	168	40.0	31	1	US-08-614-935-54 Sequence 54, Appli
25	168	40.0	31	2	US-09-130-287-53 Sequence 53, Appli
26	168	40.0	31	2	US-09-130-287-54 Sequence 54, Appli
27	160	38.1	166	1	US-08-614-935-30 Sequence 30, Appli

28	160	38.1	166	2	US-09-130-287-30	Sequence 30, Appli
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31	139	33.1	31	1	US-08-614-935-57	Sequence 57, Appli
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38	126	30.0	32	2	US-09-130-287-48	Sequence 48, Appli
39	125	29.8	31	1	US-08-614-935-58	Sequence 58, Appli
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42	124	29.5	32	1	US-08-614-935-49	Sequence 49, Appli
43	124	29.5	32	2	US-09-130-287-49	Sequence 49, Appli
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ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
; US-08-419-414-9

Query Match 100.0%; Score 420; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.5e-38; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLGCVHTACKYGLSKPNCNKKVSVYGLTKQEKQDILKEHNDPROKIARGLE 60
DB 1 NNYCKIKCLGCVHTACKYGLSKPNCNKKVSVYGLTKQEKQDILKEHNDPROKIARGLE 60

QY 61 TRGNPGPOPPAKNMKN 76
DB 61 TRGNPGPOPPAKNMKN 76

RESULT 2
ID - VAS VESVU STANDARD; PRT; 227 AA.
AC Q05110; Q0UB91;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (Ag5) (Allergen Ves v 5) (Ves v V).
OS Vespa vulgaris (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7454;
RN (1) _
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RX TISSUE=Venom;
RZ MEDLINE=93203603; PubMed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets.";
RL J. Immunol. 150:2823-2830 (1993).
RN (2)
RP NUCLEOTIDE SEQUENCE OF 24-227.
RA Suck R., Hagen S., Fiebig H.;
RT "Molecular cloning of a genomic sequence from the venom allergen antigen 5 from Vespula vulgaris";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted, wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DR EMBL; M98858; AAA30333.1; -; mRNA.
DR EMBL; AJ238849; CAB42887.1; -; Genomic_DNA.
DR PDB; 1QNX; X-ray; A=24-227.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF0188; SCP; 1.
DR PRINTS; PR00838; V5ALLERGEN.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; CRISP_1; 1.
DR PROSITE; PS01010; CRISP_2; 1.
KW 3D-structure; Allergen; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 227 Venom allergen 5.
FT DISULFID 27 40 By similarity.
FT DISULFID 31 124 By similarity.
FT DISULFID 49 117 By similarity.
FT DISULFID 193 210 By similarity.
FT CONFLICT 109 109 V -> I (in Ref. 2).
FT CONFLICT 118 118 Q -> E (in Ref. 2).
FT CONFLICT 173 173 D -> N (in Ref. 2).
FT CONFLICT 219 219 M -> K (in Ref. 2).

FT HELIX 26 28
FT TURN 32 33
FT HELIX 38 41
FT STRAND 53 57
FT HELIX 61 79
FT TURN 80 81
FT TURN 87 88
FT STRAND 94 94
FT STRAND 101 102
FT HELIX 104 114
FT TURN 115 116
FT STRAND 133 141
FT HELIX 149 157
FT HELIX 158 162
FT TURN 165 166
FT TURN 169 171
FT HELIX 174 183
FT TURN 184 184
FT TURN 186 187
FT STRAND 190 200
FT TURN 201 202
FT STRAND 203 213
FT TURN 219 220
FT STRAND 226 227
SQ SEQUENCE 227 AA; 25798 MW; 99E9813740A66F55 CRC64;

Query Match 100.0%; Score 420; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.1e-38;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLGCVHTACKYGLSKPNCNKKVSVYGLTKQEKQDILKEHNDPROKIARGLE 60
DB 24 NNYCKIKCLGCVHTACKYGLSKPNCNKKVSVYGLTKQEKQDILKEHNDPROKIARGLE 83

QY 61 TRGNPGPOPPAKNMKN 76
DB 84 TRGNPGPOPPAKNMKN 99

RESULT 3
ID - VAS VESPE STANDARD; PRT; 204 AA.
AC P35785;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Ag5) (Allergen Ves p 5) (Ves p V).
OS Vespula pensylvanica (Western yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30213;
RN (1) _
RP PROTEIN SEQUENCE.
RZ TISSUE=Venom;
RZ MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity";
RL J. Allergy Clin. Immunol. 92:707-716 (1993).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DR PIR; C44583; C44583.
DR HSP; Q05110; 1QNX.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 112.26 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLKGHVHTACKY.....RGLTRGNPGQPAPKMKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420	100.0	204	1 VA5_VESFL	P35783 vespula fla
2	420	100.0	204	1 VA5_VESVU	Q05110 vespula vul
3	416	99.0	204	1 VA5_VESPE	P35785 vespula pen
4	414	98.6	204	1 VA5_VESMC	P35760 vespula mac
5	397	94.5	204	1 VA5_VESGE	P35784 vespula ger
6	347.5	82.7	206	1 VA5_VESVI	P35787 vespula vid
7	345.5	82.3	205	1 VA5_VESSQ	P35786 vespula squ
8	306	72.9	202	1 VA51_VESCR	P35781 vespa crabr
9	306	72.9	202	1 VA52_VESCR	P35782 vespa crabr
10	305	72.6	227	1 VA52_DOLMA	P10736 dolichovep
11	296.5	70.6	203	1 VA5_DOLAR	Q05108 dolichovep
12	295	70.2	202	1 VA5_VESMA	P81657 vespa manda
13	287	68.3	215	1 VA53_SOLIN	P10737 dolichovep
14	262	62.4	206	1 VA5_DOLGA	P83377 polistes ga
15	260	61.9	206	1 VA5_POLDO	P81656 polistes do
16	260	61.9	227	2 Q68KJ8_POLDO	Q68KJ8 polistes do
17	250	59.5	205	1 VA5_POLFU	P35780 polistes fu
18	243	57.9	205	1 VA5_POLEX	P35759 polistes ex
19	243	57.9	209	1 VA5_POLAN	Q05109 polistes an
20	240	57.1	226	2 Q68KJ9_POLEX	Q68KJ9 polistes ex
21	231.5	55.1	207	1 VA5_POFSR	Q72156 polybia scu
22	156	37.1	211	1 VA3_SOIRI	P35779 solenopsis
23	156	37.1	234	1 VA3_SOLIN	P35778 solenopsis
24	92	21.9	271	2 Q9XZ44_LUTLO	Q9XZ44 lutomyia l
25	91	21.7	392	2 Q9VFY2_DROCE	Q9VFY2 drosophila
26	89	21.2	424	2 Q9XZ41_ANCCA	Q9XZ41 ancylostoma
27	88	21.0	122	2 O44205_MEGSC	O44205 megaselia s
28	88	21.0	135	2 O44206_MEGSC	O44206 megaselia s
29	88	21.0	424	2 Q76744_NECAM	Q76744 necator ame
30	87.5	20.8	255	2 Q8T9W0_AEDAE	Q8T9W0 aedes aegypt
31	86.5	20.6	255	2 Q5MIV5_AEDAL	Q5MIV5 aedes albop

32	86	20.5	424	1 ASP_ANCCA	Q16937 ancylostoma
33	84.5	20.1	248	2 Q9BIQ6_9BILA	Q9BIQ6 cooperia pu
34	84.5	20.1	248	2 Q9BIQ8_9BILA	Q9BIQ8 cooperia pu
35	84	20.0	425	2 Q816X0_9BILA	Q816X0 ancylostoma
36	83.5	19.9	217	2 Q7ZIH2_9BILA	Q7ZIH2 ancylostoma
37	82.5	19.6	459	2 Q45132_HAECCO	O45132 haemonchus
38	80.5	19.2	253	2 Q7PRE8_ANOGA	Q7PRE8 anopheles g
39	80.5	19.2	260	2 Q7PCG9_ANOGA	Q7PCG9 anopheles g
40	80.5	19.2	491	2 Q9BIQ4_9BILA	Q9BIQ4 cooperia pu
41	80	19.0	425	2 Q77153_9BILA	Q77153 ancylostoma
42	79	18.8	256	2 Q5MIT3_AEDAL	Q5MIT3 aedes albop
43	78.5	18.7	113	2 Q4QQ77_DROCE	Q4QQ77 drosophila
44	78.5	18.7	263	2 Q8ML52_DROME	Q8ML52 drosophila
45	78.5	18.7	307	2 Q7RA91_PLAYO	Q7RA91 plasmodium

ALIGNMENTS

RESULT 1

VA5_VESFL
ID - VA5_VESFL STANDARD; PRT; 204 AA.
AC P35783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).
OS Vespula flavopilosa (Yellow Jacket) (Waep).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megoptera; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30211;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hofman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- FUNCTION: May have an ancestral function in the promotion of ovum
CC fertilization by sperm.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A44583; A44583.
CC HSSP; Q05110; IQNX.
CC SMR; P35783; 1-204.
CC InterPro; IPR002413; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; VSALLERGEN.
CC PRINTS; PR00837; V5TPXLIKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; CRISP_1; 1.
CC PROSITE; PS01010; CRISP_2; 1.
KW Allergen; Direct protein sequencing.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 101 By similarity.
FT DISULFID 26 94 By similarity.
FT DISULFID 170 187 By similarity.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;

Query Match

100.0%; Score 420; DB 1; Length 204;

Db 1 NNYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Qy 61 TRGNPGPPPPAKNMKN 76
Db 61 TRGNPGPPPPAKNMKN 76

RESULT 3

B37329
antigen 5 - eastern yellowjacket
C:Species: Vespula maculifrons (eastern yellowjacket)
C:Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B37329
R:Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A:Reference number: A37329
A:Accession: B37329
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <LUI>
A:Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 98.6%; Score 414; DB 2; Length 204;
Best Local Similarity 98.7%; Pred. No. 4.5e-37;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Db 1 NNYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Qy 61 TRGNPGPPPPAKNMKN 76
Db 61 TRGNPGPPPPAKNMKN 76

RESULT 4

B44583
venom allergen antigen Ves g 5 - German yellowjacket
C:Species: Vespula germanica (German yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; A44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 94.5%; Score 397; DB 2; Length 204;
Best Local Similarity 94.7%; Pred. No. 3e-35;
Matches 72; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Db 1 NNYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Qy 61 TRGNPGPPPPAKNMKN 76
Db 61 TRGNPGPPPPAKNMKN 76

RESULT 5

B44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C:Species: Vespula vidua
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; E44522

R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-206 <HOF>
A:Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 82.7%; Score 347.5; DB 2; Length 206;
Best Local Similarity 82.9%; Pred. No. 6.3e-30;
Matches 63; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 2 NYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Db 3 NYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 62
Qy 61 TRGNPGPPPPAKNMKN 76
Db 63 TRGNPGPPPPAKNMKN 78

RESULT 6

D44583
venom allergen antigen Ves g 5 - southern yellowjacket
C:Species: Vespula squamosa (southern yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: D44583; D4522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: D44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <HOF>
A:Cross-references: UNIPROT:P35786; UNIPARC:UPI0000138094
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 82.3%; Score 345.5; DB 2; Length 205;
Best Local Similarity 82.9%; Pred. No. 1e-29; 7; Indels 1; Gaps 1;

Qy 2 NYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 60
Db 2 DYCKIKLKGCVHTACKYGLKPCNGKIVVSYGLTKQEKDILKEHNDPRQKIARGLE 61
Qy 61 TRGNPGPPPPAKNMKN 76
Db 62 TRGNPGPPPPAKNMKN 77

RESULT 7

H44583
venom allergen antigen Vesp c 5.02 - European hornet
C:Species: Vespula crabro (European hornet)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: H44583; H4522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: H44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-202 <HOF>
A:Cross-references: UNIPROT:P35782; UNIPARC:UPI0000138080
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 72.9%; Score 306; DB 2; Length 202;
Best Local Similarity 74.7%; Pred. No. 1.8e-25;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 15.9542 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLKGCVHTACKYG.....RGLTRNGPGPPAKNMKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	204	2 A44583	venom allergen ant
2	416	99.0	204	2 A44583	venom allergen ant
3	414	98.6	204	2 B37329	antigen 5 - easter
4	397	94.5	204	2 B44583	venom allergen ant
5	347.5	82.7	206	2 E44583	venom allergen ant
6	345.5	82.3	205	2 D44583	venom allergen ant
7	306	72.9	202	2 H44583	venom allergen ant
8	306	72.9	202	2 G44583	venom allergen ant
9	305	72.6	227	2 A31085	antigen 5-2 precu
10	289	68.8	213	2 B31085	antigen 5-3 precu
11	250	59.5	205	2 F44583	venom allergen ant
12	243	57.9	205	2 A37329	antigen 5 - paper
13	156	37.1	211	2 B58853	venom allergen Sol
14	156	37.1	212	2 B37330	venom allergen III
15	75	17.9	202	2 AE1278	phosphoribosyl ant
16	74	17.6	737	1 KIMSC	protein kinase C (
17	74	17.6	737	1 KIMTCE	protein kinase C (
18	73	17.4	385	2 T21763	hypothetical prote
19	70.5	16.8	2500	2 G71609	hypothetical prote
20	69.5	16.5	401	2 G96972	hypothetical prote
21	69	16.4	434	2 AE1326	hypothetical prote
22	68	16.2	605	2 F71724	aspartate-tRNA lig
23	67	15.0	2025	2 D86201	protein F12K11.6 [
24	65.5	15.6	1295	2 A32901	glpl protein precu
25	65.5	15.6	2871	2 A55567	fibrillin I - bovi
26	65.5	15.6	2871	2 A55624	fibrillin-1 precu
27	65.5	15.6	3002	2 A47221	fibrillin 1 precu
28	65	15.5	615	2 C97723	aspartate-tRNA lig
29	65	15.5	737	1 S28942	protein kinase C (

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-37;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKNKVVSGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKNKVVSGLTKQEKQDILKEHNDFRQKIARGLE 60
QY 61 TRGNPGPOPAPAKNMKN 76
DB 61 TRGNPGPOPAPAKNMKN 76

RESULT 2

A44583
venom allergen antigen Ves p 5 - western yellowjacket
C:Species: Vespula pennsylvanica (western yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: C44583; C44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: C44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 99.0%; Score 416; DB 2; Length 204;
Best Local Similarity 97.4%; Pred. No. 2.7e-37;
Matches 74; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKNKVVSGLTKQEKQDILKEHNDFRQKIARGLE 60

hypothetical prote
hypothetical prote
protein phosphatas
MADS box protein A
conserved hypothet
protein kinase C (

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XX SQ Sequence 76 AA;
Query Match 100.0%; Score 420; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.7e-45;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKGVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKGVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60

QY 61 TRGNPGPQPPAKNMKN 76
DB 61 TRGNPGPQPPAKNMKN 76

RESULT 2
AAW35688
ID AAW35688 standard; peptide; 204 AA.
AC AAW35688;
DT 13-MAY-1998 (first entry)
XX Vespid antigen 5s from Vesputa vulgaris (yellowjacket).
DE Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW vespid venom; white face hornet wasp; immunodominant peptide; T cell.
XX Vesputa vulgaris.
OS WO9733910-A1.
PN 18-SEP-1997.
XX 11-MAR-1997; 97WO-US003753.
PR 11-MAR-1996; 96US-00614935.
XX (UYRQ) UNIV ROCKEFELLER.
PI King TP;
XX WPI; 1997-470817/43.
DR Vespid venom antigen 5 peptide fragments - useful to treat or diagnose
PT vespid venom sensitivity.
XX Example 1; Fig 1; 73pp; English.
CC This sequence represents vespid antigen 5S from yellowjacket. The
CC invention relates to peptides derived from vespid venom antigen 5 (VVS)
CC that are antigenic for T cell proliferation in mice immunised with VVS.
CC The peptides can be used to treat or diagnose vespid venom sensitivity
CC e.g. to Dolichovesputa maculata (white face hornet), Vesputa vulgaris
CC (yellowjacket), V. maculifrons (yellowjacket), D. arenaria (yellow
CC hornet), Polistes amularis (wasp), P. exclamans (wasp), V. crabo
CC (European hornet), V. flavopilosa (yellowjacket), V. germanica
CC (yellowjacket), V. pennsylvanica (yellowjacket), V. squamosa
CC (yellowjacket), V. vidua (yellowjacket) and P. fuscatus (paperwasp)
XX SQ Sequence 204 AA;
Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKGVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKGVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60

QY 61 TRGNPGPQPPAKNMKN 76
DB 61 TRGNPGPQPPAKNMKN 76

RESULT 4
ABG66983
ID ABG66983 standard; protein; 204 AA.
XX AC ABG66983;
XX
```

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DB 61 TRGNPGPQPPAKNMKN 76

RESULT 3
AAV45217
ID AAV45217 standard; protein; 204 AA.
XX AC AAV45217;
DT 05-JAN-2000 (first entry)
XX Wild type wasp Ves v 5 protein sequence.
XX Bet v 1; Ves v 5; pollen allergen; Fagales; Oleales; Pinales; mutant;
KW Hymenoptera; IgE; immunoglobulin E; vaccine; allergic reaction.
XX Vesputa lewisii.
OS WO9947680-A1.
PN 23-SEP-1999.
XX 16-MAR-1999; 99WO-DK000136.
PR 16-MAR-1998; 98DK-00000364.
XX (ALKA-) ALK-ABELLO AS.
PI Ipsen HH, Spangfort MD, Larsen JN;
XX WPI; 1999-601103/51.
DR N-PSDB; AAZ25685.
XX New mutated allergen with lower specific affinity to IgE, useful for
PT treatment of allergic reactions.
XX Example 1; Fig 13; 77pp; English.
CC The present invention describes a recombinant mutated allergen, with a
CC surface exposed substituted amino acid on a B-cell epitope. The
CC recombinant, non-natural, mutated allergen has at least one surface-
CC exposed conserved amino acid of a B-cell epitope substituted by another
CC amino acid, and essentially the same alpha-carbon backbone tertiary
CC structure as the naturally occurring allergen. The substituted amino acid
CC does not occur in the same position of any known homologous protein
CC within the taxonomic order of the natural allergen. Specific IgE binding
CC to the mutant is reduced compared to the naturally occurring allergen.
CC The recombinant allergen is used as a vaccine to treat, prevent or
CC alleviate allergic reactions. The present sequence represents the wild
CC type Ves v 5, which can have the following mutations: Lys72Ala and
CC Ty-96Ala
XX SQ Sequence 204 AA;
Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKGVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKGVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60

QY 61 TRGNPGPQPPAKNMKN 76
DB 61 TRGNPGPQPPAKNMKN 76

RESULT 4
ABG66983
ID ABG66983 standard; protein; 204 AA.
XX AC ABG66983;
XX
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 105.878 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-95

Perfect score: 420

Sequence: 1 NNYCKIKLKGVTACKYGV.....RGLETRGNPGPQPPAKNMKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	76	AAE28829	Aae28829 Vesputa v
2	420	100.0	204	Aaw35688	Aaw35688 Vespid an
3	420	100.0	204	Aay45217	Aay45217 Wild type
4	420	100.0	204	ABG66983	ABG66983 Wasp veno
5	420	100.0	204	ABG67052	ABG67052 Wasp veno
6	420	100.0	204	ABG67104	ABG67104 Wasp veno
7	420	100.0	204	Aae28820	Aae28820 Vesputa v
8	420	100.0	209	Abm00031	Abm00031 Allergen
9	420	100.0	227	Aay25644	Aay25644 Vesputa s
10	420	100.0	227	ADC34893	ADC34893 Wasp alie
11	414	98.6	204	Aaw35687	Aaw35687 Vespid an
12	414	98.6	204	ABG66977	ABG66977 Wasp veno
13	414	98.6	204	ABG67103	ABG67103 Wasp veno
14	411	97.9	227	AAE13071	AAE13071 Vesputa v
15	347.5	82.7	206	Aay25648	Aay25648 Vesputa s
16	347.5	82.7	206	ADC34897	ADC34897 Wasp alie
17	313	74.5	57	AAE28828	Aae28828 Vesputa v
18	305	72.6	204	Aaw35691	Aaw35691 Vespid an
19	296.5	70.6	203	Aaw35689	Aaw35689 Vespid an
20	289	68.8	205	AAW35690	AAW35690 Vespid an
21	279	66.4	50	AAE28827	Aae28827 Vesputa v
22	254	60.5	46	AAE28812	Aae28812 Vesputa v
23	243	57.9	205	AAW35693	AAW35693 Vespid an
24	243	57.9	205	AAW35692	AAW35692 Vespid an

25	243	57.9	205	5	AAE28821	Aae28821 Polistes
26	220	52.4	33	5	AAE28811	Aae28811 Vesputa v
27	184	43.8	32	5	AAE28810	Aae28810 Vesputa v
28	180	42.9	31	2	AAW35648	Aaw35648 T cell pe
29	174	41.4	31	2	AAW35647	Aaw35647 T cell pe
30	168	40.0	31	2	AAW35656	Aaw35656 T cell pe
31	168	40.0	31	2	AAW35655	Aaw35655 T cell pe
32	153	36.4	162	5	AAE21099	Aae21099 Human epe
33	147	35.0	172	4	ABU53238	ABU53238 Human tes
34	142	33.8	31	2	AAW35657	Aaw35657 T cell pe
35	140	33.3	24	5	AAE28809	Aae28809 Vesputa v
36	139	33.1	31	2	AAW35659	Aaw35659 T cell pe
37	136	32.4	31	2	AAW35658	Aaw35658 T cell pe
38	135	32.1	30	2	AAW35645	Aaw35645 Immunomod
39	126	30.0	32	2	AAW35650	Aaw35650 T cell pe
40	125	29.8	31	2	AAW35660	Aaw35660 T cell pe
41	125	29.8	31	2	AAW35661	Aaw35661 T cell pe
42	124	29.5	32	2	AAW35651	Aaw35651 T cell pe
43	119	28.3	32	2	AAW35644	Aaw35644 Immunomod
44	112.5	26.8	31	2	AAW35649	Aaw35649 T cell pe
45	107	25.5	18	5	AAE28808	Aae28808 Vesputa v

ALIGNMENTS

RESULT 1

AAE28829	AAE28829 standard; peptide; 76 AA.
XX	XX
AC	AAE28829;
XX	XX
DT	27-DEC-2002 (first entry)
XX	XX
DE	Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #16.
XX	XX
KW	Allergen; hybrid protein; allergenicity; immune system related disease;
KW	immunogenicity; allergy; vaccine; antigen 5.
XX	XX
OS	Vesputa vulgaris.
XX	XX
PN	WO200270665-A2.
XX	XX
PD	12-SEP-2002.
XX	XX
PF	04-MAR-2002; 2002WO-US006765.
XX	XX
PR	02-MAR-2001; 2001US-0272818P.
XX	XX
PA	(UYRQ) UNIV ROCKEFELLER.
PA	(ALKA-) ALK-ABELLO AS.
XX	XX
PI	King TP, Spangfort MD;
XX	XX
WPI	WPI; 2002-698751/75.
DR	N-PSDB; AAD46274.
XX	XX
PT	New allergen hybrid protein having reduced allergenicity but retaining
PT	immunogenicity, useful for treating allergy or immune system related
XX	XX
PS	Claim 17; Page 152; 222pp; English.
XX	XX
CC	The present invention relates to recombinant allergen hybrid proteins
CC	having reduced allergenicity but retaining immunogenicity. The hybrid
CC	proteins comprise a peptide epitope sequence of an allergen protein and a
CC	scaffold protein that is structurally homologous to the allergen protein.
CC	Sequences of the invention comprise a native conformation and the peptide
CC	epitope sequence is present in a surface accessible region of the hybrid
CC	protein corresponding to its position in the allergen protein. The hybrid
CC	proteins are useful for treating allergy or immune system related
CC	diseases. They are also used as vaccines. The present sequence is Vesputa
CC	vulgaris antigen 5 (Ves V5) allergen peptide

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 12.4046 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLGGVHTACKYK.....VVSGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /SID55/ptodata/2/pubpaa/US03_NEW_PUB pep.*
6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	100.0	227	6	US-10-498-026-76
2	215.5	77.2	206	6	US-10-498-026-80
3	65.5	23.5	2871	7	US-11-169-041-131
4	65.5	23.5	3002	6	US-10-821-234-916
5	64	22.9	271	6	US-10-533-811-1
6	61.5	22.0	298	7	US-11-124-367A-416
7	61.5	22.0	298	7	US-11-124-367A-417
8	61.5	22.0	298	7	US-11-124-367A-419
9	61.5	22.0	313	7	US-11-124-367A-418
10	61.5	22.0	416	7	US-11-124-367A-415
11	58	20.8	2911	7	US-11-090-617-706
12	56	20.1	365	7	US-11-108-528-56
13	56	20.1	365	7	US-11-108-528-58
14	54.5	19.5	236	6	US-10-527-500-65
15	54.5	19.5	277	6	US-10-527-500-23
16	54.5	19.5	543	7	US-11-106-672A-10
17	54.5	19.5	543	7	US-11-057-732-6
18	54.5	19.5	543	7	US-11-154-805A-5
19	54.5	19.5	592	7	US-11-106-672A-14
20	54	19.4	135	7	US-11-188-298-3692
21	54	19.4	245	7	US-11-188-298-8231
22	54	19.4	336	7	US-11-188-298-7686
23	54	19.4	1294	7	US-11-079-463-7534
24	53	19.0	253	7	US-11-172-740-561
25	52.5	18.8	996	7	US-11-079-463-6193

26	52	18.6	254	7	US-11-172-740-2285	Sequence 2285, Ap
27	52	18.6	254	7	US-11-188-298-19953	Sequence 19953, A
28	52	18.6	618	7	US-11-033-116-2	Sequence 2, Appl
29	52	18.6	1978	7	US-11-212-443-60	Sequence 60, Appl
30	51.5	18.5	199	6	US-10-793-626-1342	Sequence 1342, Ap
31	51.5	18.5	251	6	US-10-793-626-3050	Sequence 3050, Ap
32	51.5	18.5	299	7	US-11-188-298-17281	Sequence 17281, A
33	51	18.3	357	7	US-11-108-528-60	Sequence 60, Appl
34	51	18.3	357	7	US-11-108-528-62	Sequence 62, Appl
35	51	18.3	604	7	US-11-079-463-5436	Sequence 5436, Ap
36	51	18.3	643	7	US-11-096-568A-18660	Sequence 18660, A
37	51	18.3	851	7	US-11-096-568A-18659	Sequence 18659, A
38	51	18.3	872	7	US-11-096-568A-18658	Sequence 18658, A
39	50.5	18.1	320	7	US-11-079-463-8514	Sequence 8514, Ap
40	50	17.9	245	7	US-11-188-298-13741	Sequence 13741, A
41	50	17.9	342	6	US-10-491-468-8	Sequence 8, Appl
42	50	17.9	342	6	US-10-491-468-40	Sequence 40, Appl
43	50	17.9	381	6	US-10-689-742-172	Sequence 172, App
44	50	17.9	408	6	US-10-491-468-13	Sequence 13, Appl
45	50	17.9	408	7	US-11-072-512-2081	Sequence 2081, Ap

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76
Query Match 100.0%; Score 279; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLGGVHTACKYGLKPCNGKVVSVYGLTKQEKQDILKEHND 50
Db 24 NNYCKIKLGGVHTACKYGLKPCNGKVVSVYGLTKQEKQDILKEHND 73

RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80
Query Match 77.2%; Score 215.5; DB 6; Length 206;
Best Local Similarity 80.0%; Pred. No. 7.6e-21;
Matches 40; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

ORGANISM: Vesputula vulgaris
US-10-091-135-94

Query Match 100.0%; Score 279; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50

RESULT 3
US-10-091-135-95
Sequence 95, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
LENGTH: 76
TYPE: PRT
ORGANISM: Vesputula vulgaris
US-10-091-135-95

Query Match 100.0%; Score 279; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-28;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50

RESULT 4
US-10-001-245-119
Sequence 119, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 119
LENGTH: 201
TYPE: PRT
ORGANISM: Vesputula
NAME/KEY: MISC FEATURE
LOCATION: (1)-(201)
OTHER INFORMATION: where x is any amino acid
US-10-001-245-119

Query Match 100.0%; Score 279; DB 4; Length 201;

Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50

RESULT 5
US-10-001-245-117
Sequence 117, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 117
LENGTH: 202
TYPE: PRT
ORGANISM: Vesputula
NAME/KEY: MISC FEATURE
LOCATION: (1)-(202)
OTHER INFORMATION: where x is any amino acid
US-10-001-245-117

Query Match 100.0%; Score 279; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKCLKGGVHTACKYGLKPCGKGVVSYGLTKQEKQDILKEHND 50

RESULT 6
US-10-001-245-118
Sequence 118, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 118
LENGTH: 203
TYPE: PRT
ORGANISM: Vesputula
NAME/KEY: MISC FEATURE
LOCATION: (1)-(203)
OTHER INFORMATION: where x is any amino acid
US-10-001-245-118

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 76.5267 Seconds
(without alignments)
272.996 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLGGVHTACKY.....VVSGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	279	100.0	50	4	US-10-091-135-93	Sequence 93, Appl	
2	279	100.0	57	4	US-10-091-135-94	Sequence 94, Appl	
3	279	100.0	76	4	US-10-091-135-95	Sequence 95, Appl	
4	279	100.0	201	4	US-10-001-245-119	Sequence 119, Appl	
5	279	100.0	202	4	US-10-001-245-117	Sequence 117, Appl	
6	279	100.0	203	4	US-10-001-245-118	Sequence 118, Appl	
7	279	100.0	204	3	US-09-847-208-162	Sequence 162, Appl	
8	279	100.0	204	4	US-10-091-135-16	Sequence 16, Appl	
9	279	100.0	204	4	US-10-091-135-64	Sequence 64, Appl	
10	279	100.0	204	4	US-10-091-135-65	Sequence 65, Appl	
11	279	100.0	204	4	US-10-091-135-81	Sequence 81, Appl	
12	279	100.0	204	4	US-10-719-553-39	Sequence 39, Appl	
13	279	100.0	209	3	US-09-957-806A-22	Sequence 22, Appl	
14	279	100.0	210	4	US-10-001-245-214	Sequence 214, Appl	
15	279	100.0	227	3	US-09-847-208-170	Sequence 170, Appl	
16	279	100.0	227	5	US-10-809-689-82	Sequence 82, Appl	
17	275	98.6	204	3	US-09-847-208-166	Sequence 166, Appl	
18	275	98.6	204	4	US-10-091-135-66	Sequence 66, Appl	
19	273	97.8	204	3	US-09-847-208-165	Sequence 165, Appl	
20	273	97.8	204	4	US-10-091-135-63	Sequence 63, Appl	
21	264.5	94.8	194	4	US-10-001-245-120	Sequence 120, Appl	
22	258.5	92.7	198	4	US-10-001-245-121	Sequence 121, Appl	
23	256	91.8	204	3	US-09-847-208-163	Sequence 163, Appl	
24	256	91.8	204	4	US-10-091-135-67	Sequence 67, Appl	
25	254	91.0	46	4	US-10-091-135-6	Sequence 6, Appl	
26	227	81.4	192	4	US-10-001-245-122	Sequence 122, Appl	
27	220	78.9	39	4	US-10-091-135-5	Sequence 5, Appl	

28	215.5	77.2	205	3	US-09-847-208-167	Sequence 167, Appl
29	215.5	77.2	205	4	US-10-091-135-69	Sequence 69, Appl
30	215.5	77.2	206	3	US-09-847-208-171	Sequence 171, Appl
31	215.5	77.2	206	4	US-10-091-135-68	Sequence 68, Appl
32	215.5	77.2	206	5	US-10-809-689-86	Sequence 86, Appl
33	190	68.1	204	4	US-10-091-135-70	Sequence 70, Appl
34	190	68.1	227	3	US-09-847-208-90	Sequence 90, Appl
35	189.5	67.9	166	4	US-10-001-245-124	Sequence 124, Appl
36	184	65.9	32	4	US-10-091-135-4	Sequence 4, Appl
37	183.5	65.8	170	4	US-10-001-245-123	Sequence 123, Appl
38	182	65.2	202	3	US-09-847-208-160	Sequence 160, Appl
39	182	65.2	202	3	US-09-847-208-161	Sequence 161, Appl
40	182	65.2	202	4	US-10-091-135-74	Sequence 74, Appl
41	182	65.2	202	4	US-10-091-135-75	Sequence 75, Appl
42	177	63.4	202	3	US-09-847-208-172	Sequence 172, Appl
43	177	63.4	202	4	US-10-091-135-73	Sequence 73, Appl
44	171.5	61.5	203	3	US-09-847-208-86	Sequence 86, Appl
45	171.5	61.5	203	4	US-10-091-135-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-10-091-135-93
; Sequence 93, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGI
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Vesputia vulgaris
US-10-091-135-93

Query Match	100.0%	Score 279;	DB 4;	Length 50;
Best Local Similarity	100.0%	Pred. No. 4.1e-28;		
Matches	50;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
Qy	1	NNYCKIKLGGVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND	50	
Db	1	NNYCKIKLGGVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND	50	

RESULT 2
US-10-091-135-94
; Sequence 94, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGI
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 57
; TYPE: PRT

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DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 2
US-08-614-935-2
Sequence 2, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE: Vespula vulgaris
US-08-614-935-2
Query Match 100.0%; Score 279; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50
RESULT 3
US-09-130-287-2
Sequence 2, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE: Vespula vulgaris
US-09-130-287-2
Query Match 100.0%; Score 279; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50
RESULT 4
US-09-541-759-6
Sequence 6, Application US/09541759
Patent No. 6723322
GENERAL INFORMATION:
APPLICANT: Lustigman, Sara
APPLICANT: Pearlman, Eric
APPLICANT: Umasch, Thomas
TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
FILE REFERENCE: 63475/252
CURRENT APPLICATION NUMBER: US/09/541,759
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent in version 3.0
SEQ ID NO 6
LENGTH: 227
TYPE: PPT
ORGANISM: Vespula vulgaris
US-09-541-759-6
Query Match 100.0%; Score 279; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 15.0763 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-93

Perfect score: 279

Sequence: 1 NNYKIKLKGVTACKYG.....VVSYGLTKQEKQDKLKEHND 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	279	100.0	204	1 US-08-419-414-9	Sequence 9, Appl
2	279	100.0	204	1 US-08-614-935-2	Sequence 2, Appl
3	279	100.0	204	2 US-09-130-287-2	Sequence 2, Appl
4	279	100.0	227	2 US-09-541-759-6	Sequence 6, Appl
5	273	97.8	204	1 US-08-614-935-1	Sequence 1, Appl
6	273	97.8	204	2 US-09-130-287-1	Sequence 1, Appl
7	190	68.1	204	1 US-08-614-935-5	Sequence 5, Appl
8	190	68.1	204	2 US-09-130-287-5	Sequence 5, Appl
9	180	64.5	31	1 US-08-614-935-46	Sequence 46, Appl
10	180	64.5	31	2 US-09-130-287-46	Sequence 46, Appl
11	174	62.4	31	1 US-08-614-935-45	Sequence 45, Appl
12	174	62.4	31	2 US-09-130-287-45	Sequence 45, Appl
13	171.5	61.5	203	1 US-08-419-414-8	Sequence 8, Appl
14	171.5	61.5	203	2 US-08-614-935-3	Sequence 3, Appl
15	171.5	61.5	203	1 US-09-130-287-3	Sequence 3, Appl
16	163	58.4	205	1 US-08-614-935-4	Sequence 4, Appl
17	163	58.4	205	2 US-09-130-287-4	Sequence 4, Appl
18	137	49.1	205	1 US-08-419-414-10	Sequence 10, Appl
19	137	49.1	205	1 US-08-614-935-6	Sequence 6, Appl
20	137	49.1	205	1 US-08-614-935-7	Sequence 7, Appl
21	137	49.1	205	2 US-09-130-287-6	Sequence 6, Appl
22	137	49.1	205	2 US-09-130-287-7	Sequence 7, Appl
23	126	45.2	32	1 US-08-614-935-48	Sequence 48, Appl
24	126	45.2	32	2 US-09-130-287-48	Sequence 48, Appl
25	124	44.4	32	1 US-08-614-935-49	Sequence 49, Appl
26	124	44.4	32	2 US-09-130-287-49	Sequence 49, Appl
27	119	42.7	32	1 US-08-614-935-42	Sequence 42, Appl

28 119 42.7 32 2 US-09-130-287-42 Sequence 42, Appl
29 112.5 40.3 31 1 US-08-614-935-47 Sequence 47, Appl
30 112.5 40.3 31 2 US-09-130-287-47 Sequence 47, Appl
31 94 33.7 34 1 US-08-614-935-50 Sequence 50, Appl
32 94 33.7 34 1 US-08-614-935-51 Sequence 51, Appl
33 94 33.7 34 2 US-09-130-287-50 Sequence 50, Appl
34 94 33.7 34 2 US-09-130-287-51 Sequence 51, Appl
35 88.5 31.7 20 1 US-08-614-935-8 Sequence 8, Appl
36 88.5 31.7 20 2 US-09-130-287-8 Sequence 8, Appl
37 76.5 27.4 20 1 US-08-614-935-9 Sequence 9, Appl
38 76.5 27.4 20 2 US-09-130-287-9 Sequence 9, Appl
39 73 26.2 20 1 US-08-614-935-10 Sequence 10, Appl
40 73 26.2 20 2 US-09-130-287-10 Sequence 10, Appl
41 72.5 26.0 34 1 US-08-614-935-33 Sequence 33, Appl
42 72.5 26.0 34 2 US-09-130-287-33 Sequence 33, Appl
43 70 25.1 20 1 US-08-614-935-11 Sequence 11, Appl
44 70 25.1 20 2 US-09-130-287-11 Sequence 11, Appl
45 65.5 23.5 1935 2 US-09-949-016-10403 Sequence 10403, A

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/419,414
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
US-08-419-414-9

Query Match 100.0%; Score 279; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.2e-25; Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 50

RESULT 2

VA5_VESVU STANDARD; PRT; 227 AA.
AC Q05110; Q9UB91;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (Ag5) (Allergen Ves v 5) (Ves v V).
OS Vespa vulgaris (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7454;
RN (1)_TaxID=7454;
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93203603; PubMed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets.";
RL J. Immunol. 150:2823-2830(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 24-227.
RA Suck R., Hagen S., Fiebig H.;
RT "Molecular cloning of a genomic sequence from the venom allergen antigen 5 from Vespula vulgaris.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL; M98958; AAA30333.1; -; mRNA.
CC EMBL; AJ238849; CAB42887.1; -; Genomic DNA.
CC PDB; 1QNX; X-ray; A=24-227.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PR00837; V5TPXLIKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; CRISP_1; 1.
CC PROSITE; PS01010; CRISP_2; 1.
KW 3D-structure; Allergen; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 227 Venom allergen 5.
FT DISULFD 27 40 By similarity.
FT DISULFD 31 124 By similarity.
FT DISULFD 49 117 By similarity.
FT DISULFD 193 210 By similarity.
FT CONFLICT 109 109 V -> I (in Ref. 2).
FT CONFLICT 118 118 Q -> E (in Ref. 2).
FT CONFLICT 173 173 D -> N (in Ref. 2).
FT CONFLICT 219 219 M -> K (in Ref. 2).
FT HELIX 26 28
FT TURN 32 33
FT HELIX 38 41
FT STRAND 53 57

FT HELIX 61 79
FT TURN 80 81
FT TURN 87 88
FT STRAND 94 94
FT STRAND 101 102
FT HELIX 104 114
FT TURN 115 116
FT STRAND 133 141
FT HELIX 149 157
FT HELIX 158 162
FT TURN 165 166
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FT STRAND 190 200
FT TURN 201 202
FT STRAND 203 213
FT TURN 219 220
FT STRAND 226 227
SQ SEQUENCE 227 AA; 25798 MW; 99E9813740A66F55 CRC64;

Query Match 100.0%; Score 279; DB 1; Length 227;

Best Local Similarity 100.0%; Pred. No. 1.3e-25; Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 50
DB 24 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 73

RESULT 3

VA5_VESPE STANDARD; PRT; 204 AA.
AC P35785;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves p 5) (Ves p V).
OS Vespula pensylvanica (Western yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30213;
RN (1)
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hofman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC PIR; C44583; C44583.
CC HSSP; Q05110; 1QNX.
CC SMR; P35785; 1-204.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PR00837; V5TPXLIKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 73.855 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIRKLGKGVHTACKY.....VVSGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	204	1 VA5_VESFL	P35783 vespula fla
2	279	100.0	227	1 VA5_VESVU	Q05110 vespula vul
3	275	98.6	204	1 VA5_VESPE	P35785 vespula pen
4	273	97.8	204	1 VA5_VESMC	P35760 vespula mac
5	256	91.8	204	1 VA5_VESGE	P35784 vespula ger
6	215.5	77.2	205	1 VA5_VESSQ	P35786 vespula squ
7	215.5	77.2	206	1 VA5_VESVI	P35787 vespula vid
8	190	68.1	227	1 VA52_DOLMA	P10736 dolichovesp
9	182	65.2	202	1 VA51_VESCR	P35781 vespa crabr
10	182	65.2	202	1 VA52_VESCR	P35782 vespa crabr
11	177	63.4	202	1 VA5_VESMA	F81657 vespa manda
12	171.5	61.5	203	1 VA5_DOLAR	Q05108 dolichovesp
13	161	57.7	215	1 VA53_DOLMA	P10737 dolichovesp
14	146	52.3	206	1 VA5_POLGA	P83377 polistes ga
15	143	51.3	206	1 VA5_POLDO	P81656 polistes do
16	143	51.3	227	2 Q68KJ9_POLDO	Q68KJ8 polistes do
17	139	49.8	205	1 VA5_POLFU	P35780 polistes fu
18	137	49.1	205	1 VA5_POLEX	P35759 polistes ex
19	137	49.1	209	1 VA5_POLAN	Q05109 polistes an
20	134	48.0	226	2 Q68KJ9_POLEX	Q68KJ9 polistes ex
21	120.5	43.2	207	1 VA5_POLSR	Q72156 polybia scu
22	77	27.6	211	1 VA3_SOLRI	P35779 solenopsis
23	77	27.6	234	1 VA3_SOLIN	P35778 solenopsis
24	70.5	25.3	2500	2 Q96223_PLAF7	Q96223 plasmodium
25	69.5	24.9	401	2 Q97LG9_CLOAB	Q97LG9 clostridium
26	69.5	24.9	525	2 Q9DWE1_RCWMV	Q9DWE1 rat cytomeg
27	67.5	24.2	283	2 Q7Q991_ANOGA	Q7Q991 anopheles g
28	67.5	24.2	610	2 Q54FR6_DICDI	Q54FR6 dictyosteli
29	67.5	24.2	2884	2 Q4SHN1_TETNG	Q4SHN1 tetraodon n
30	67	24.0	2025	2 Q9SHK4_ARATH	Q9SHK4 arabidopsis
31	66	23.7	3429	2 Q81BP1_PLAF7	Q81BP1 plasmodium

32	65.5	23.5	195	2	Q75N89 HUMAN	Q75N89 homo sapien
33	65.5	23.5	307	2	Q7RA91_PLAYO	Q7RA91 plasmodium
34	65.5	23.5	1095	2	Q60784_MOUSE	Q60784 mus musculu
35	65.5	23.5	1295	1	GLP1_CAEEL	P13508 caenorhabdi
36	65.5	23.5	1365	2	Q75N88 HUMAN	Q75N88 homo sapien
37	65.5	23.5	2871	1	FBN1_BOVIN	P98133 bos taurus
38	65.5	23.5	2871	1	FBN1_MOUSE	P35555 homo sapien
39	65.5	23.5	2871	1	FBN1_PIG	Q61554 sus scrofa
40	65.5	23.5	2871	1	Q75N87_HUMAN	Q75N87 homo sapien
41	65.5	23.5	2871	2	Q9WU88_RAT	Q9WU88 rattus norv
42	65.5	23.5	3857	2	O88840_MOUSE	O88840 mus musculu
43	65.5	23.5	3857	2	O54YC8_DICDI	Q54YC8 dictyosteli
44	64.5	23.1	415	2	Q9XZ44_JUTLO	Q9XZ44 lutzomyia l
45	64	22.9	271	2		

ALIGNMENTS

RESULT 1
ID - VA5_VESFL STANDARD; PRT; 204 AA.
AC P35783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).
OS Vespula flavopilosa (Yellow Jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID:30211;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hofman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- FUNCTION: May have an ancestral function in the promotion of ovum
CC fertilization by sperm.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A44583; A44583.
CC HSP: Q05110; IQNX.
CC SMR: P35783; 1-204.
CC InterPro: IPR001283; Allrgn_V5/Tpx1.
CC InterPro: IPR002413; V5_allergen.
CC Pfam: PF00188; SCP; 1.
CC PRINTS: PR00838; V5ALLERGEN.
CC PRINTS: PR00837; V5TPXLIKE.
CC ProDom: PD000542; Allrgn_V5/Tpx1; 1.
CC SMART: SM00198; SCP; 1.
CC PROSITE: PS01009; CRISP_1; 1.
CC PROSITE: PS01010; CRISP_2; 1.
CC Allergen: Direct protein sequencing.
KW Allergen; By similarity.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 101 By similarity.
FT DISULFID 26 94 By similarity.
FT DISULFID 170 187 By similarity.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;
Query Match 100.0%; Score 279; DB 1; Length 204;


```
RESULT 3
B37329
antigen 5 - eastern yellowjacket
C:Species: Vespula maculifrons (eastern yellowjacket)
C:Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B37329
R:Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A:Reference number: A37329
A:Accession: B37329
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 97.8%; Score 273; DB 2; Length 204;
Best Local Similarity 98.0%; Pred. No. 7e-25;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
|||||
DB 1 NNYCKIKLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
|||||

RESULT 4
B44583
venom allergen antigen Ves g 5 - German yellowjacket
C:Species: Vespula germanica (German yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; A44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 91.8%; Score 256; DB 2; Length 204;
Best Local Similarity 92.0%; Pred. No. 7.1e-23;
Matches 46; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
|||||
DB 1 NNYCKIKLKGGVHTACKYGLSKPNCANKKVVAYGLTKQEKQDILKEHND 50
|||||

RESULT 5
D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C:Species: Vespula squamosa (southern yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: D44583; D44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: D44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <HOF>
A:Cross-references: UNIPROT:P35786; UNIPARC:UPI0000138094
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 77.2%; Score 215.5; DB 2; Length 205;
Best Local Similarity 80.0%; Pred. No. 4.4e-18;
Matches 40; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 NYCKIKLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
|||||
```

```
Db 2 DYCKIKLKGGVHTACKYGLTKPNCNGKVVVSYGVTQAEKQELKHNND 51
|||||

RESULT 6
E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C:Species: Vespula vidua
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: E44583; E44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: E44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-206 <HOF>
A:Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 77.2%; Score 215.5; DB 2; Length 206;
Best Local Similarity 80.0%; Pred. No. 4.4e-18;
Matches 40; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 NYCKIKLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
|||||
DB 3 NYCKIKLKGGVHTACKYGLTKPNCNGKVVVSYGLTKQEKQELKHNND 52
|||||

RESULT 7
A31085
antigen 5-2 precursor - bald-faced hornet
C:Species: Vespula maculata (bald-faced hornet)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A31085
R:Fang, K.S.Y.; Vitale, M.; Fehner, P.; King, T.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988
A:Title: cDNA cloning and primary structure of a white-face hornet venom allergen, ant
A:Reference number: A31085; MUID:88124947; PMID:3422469
A:Accession: A31085
A:Molecule type: mRNA
A:Residues: 1-227 <FAN>
A:Cross-references: UNIPROT:P10736; UNIPARC:UPI000013807D; GB:J03601; NID:G156714; PID:
C:Superfamily: yellowjacket venom allergen antigen 5
F:1-23/DNA: signal sequence #status predicted <SIG>
F:24-227/Product: antigen 5-2 #status predicted <MAT>

Query Match 68.1%; Score 190; DB 2; Length 227;
Best Local Similarity 68.6%; Pred. No. 5e-15;
Matches 35; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

QY 1 NNYCKIKLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
|||||
DB 24 NNYCKIKCRK-GIHTLCFGTSMKPCNGKVVVSYGLTKQEKQELKHNND 73
|||||

RESULT 8
H44583
venom allergen antigen Vesp c 5.02 - European hornet
C:Species: Vespula crabro (European hornet)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: H44583; H44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: H44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-202 <HOF>
A:Cross-references: UNIPROT:P35782; UNIPARC:UPI0000138080
C:Superfamily: yellowjacket venom allergen antigen 5
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 10.4962 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLGGVHTACKYG.....VVSYGLTKQBQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	204	2 A44583	venom allergen ant
2	275	98.6	204	2 C44583	venom allergen ant
3	273	97.8	204	2 B37329	antigen 5 - easter
4	256	91.8	204	2 B44583	venom allergen ant
5	215.5	77.2	205	2 D44583	venom allergen ant
6	215.5	77.2	206	2 A44583	antigen 5-2 precu
7	190	68.1	227	2 A31085	venom allergen ant
8	182	65.2	202	2 H44583	venom allergen ant
9	182	65.2	202	2 G44583	antigen 5-3 precu
10	163	58.4	213	2 B31085	venom allergen ant
11	139	49.8	205	2 F44583	antigen 5 - paper
12	137	49.1	205	2 A37329	venom allergen Sol
13	77	27.6	211	2 B58853	venom allergen III
14	77	27.6	212	2 B37330	hypothetical prote
15	70.5	25.3	2500	2 G71609	hypothetical prote
16	69.5	24.9	401	2 G96972	protein f12k11.6 [
17	67	24.0	2025	2 D96201	glp1 protein precu
18	65.5	23.5	1295	2 A32901	fibrillin I - bovi
19	65.5	23.5	2871	2 A55567	fibrillin-1 precu
20	65.5	23.5	2871	2 A55624	fibrillin 1 precu
21	65.5	23.5	3002	2 A47221	hypothetical prote
22	63.5	22.8	292	2 H81857	hypothetical prote
23	63.5	22.8	342	2 B1086	hypothetical prote
24	60.5	21.7	1469	2 T19459	enterotoxin D prec
25	58.5	21.0	258	2 A33953	fibrillin-2 precu
26	58.5	21.0	2907	2 A57278	probable membrane
27	58.5	21.0	4910	2 S64942	masking protein pr
28	58	20.8	1712	2 A38261	fibrillin-2 precu
29	58	20.8	2918	2 A54105	

lipopolyaccharide
probable serine/th
secreted protein p
two-component sens
hypothetical prote
PINT domain protei
nucleocapsid prote
hypothetical prote
hypothetical prote
G2-G1 polypeptide
MADS box protein A
cysteine-rich prot
acid phosphatase (
hemagglutinin-neur
minor inner core p
probable sugar-nuc

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula Flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522

R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993

A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862

A:Accession: A44583

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-204 <HOF>

A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F

C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 100.0%; Score 279; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNYCKIKLGGVHTACKYGLKPCNGKVVSVGLTKQEKQDILKEHND 50
Db 1 NNYCKIKLGGVHTACKYGLKPCNGKVVSVGLTKQEKQDILKEHND 50

RESULT 2

C44583
venom allergen antigen Ves p 5 - western yellowjacket
C:Species: Vespula pensylvanica (western yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: C44583; C44522

R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993

A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862

A:Accession: C44583

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-204 <HOF>

A:Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093

C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 98.6%; Score 275; DB 2; Length 204;
Best Local Similarity 96.0%; Pred. No. 4.1e-25;
Matches 48; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNYCKIKLGGVHTACKYGLKPCNGKVVSVGLTKQEKQDILKEHND 50
Db 1 NNYCKIKLGGVHTACKYGLKPCNGKVVSVGLTKQEKQDILKEHND 50

```

XX SQ Sequence 50 AA;
Query Match 100.0%; Score 279; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.4e-28; Mismatches 0; Indels 0; Gaps 0;
Matches 50; Conservative 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50
    |||||
DB 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50

RESULT 2
AAE28828
ID AAE28828 standard; peptide; 57 AA.
XX
AC AAE28828;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #15.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
XX WPI; 2002-698751/75.
XX DR N-PSDB; AAD46273.
XX
XX New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 57 AA;
Query Match 100.0%; Score 279; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.1e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 50; Conservative 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50
    |||||
DB 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50

RESULT 3
AAE28829

```

```

ID AAE28829 standard; peptide; 76 AA.
XX
AC AAE28829;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #16.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
XX WPI; 2002-698751/75.
XX DR N-PSDB; AAD46274.
XX
XX New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 279; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.5e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 50; Conservative 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50
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DB 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50

RESULT 4
AAW35688
ID AAW35688 standard; peptide; 204 AA.
XX
AC AAW35688;
XX
DT 13-MAY-1998 (first entry)
XX
DE Vespid antigen 5a from Vesputa vulgaris (yellowjacket).
XX
KW Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW vespid venom; white face hornet wasp; immunodominant peptide; 1 cell.
XX
OS Vesputa vulgaris.
XX
PN WO9733910-A1.

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 69.6565 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLGGVHTACKYG.....VVSYLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 21:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	50	AAE28827	Aae28827 Vesputa v
2	279	100.0	57	AAE28828	Aae28828 Vesputa v
3	279	100.0	76	AAE28829	Aae28829 Vesputa v
4	279	100.0	204	AAW35688	Aaw35688 Vespid an
5	279	100.0	204	AAW45217	Aay45217 Wild type
6	279	100.0	204	ABG66983	Abg66983 Wasp veno
7	279	100.0	204	ABG67052	Abg67052 Wasp veno
8	279	100.0	204	ABG67104	Abg67104 Wasp veno
9	279	100.0	204	ABG67103	Abg67103 Wasp veno
10	279	100.0	204	AAE28820	Aae28820 Vesputa v
11	279	100.0	209	ABM00031	Abm00031 Allergen
12	279	100.0	227	AAV25644	Aay25644 Vesputa s
13	279	100.0	227	AAE13071	Aae13071 Vesputa v
14	279	100.0	227	ADC34893	Adc34893 Wasp alle
15	273	97.8	204	AAW35687	Aaw35687 Vespid an
16	273	97.8	204	ABG66977	Abg66977 Wasp veno
17	254	91.0	46	AAE28812	Aae28812 Vesputa v
18	220	78.9	39	AAE28811	Aae28811 Vesputa s
19	215.5	77.2	206	AAV25648	Aay25648 Vesputa s
20	215.5	77.2	206	ADC34897	Adc34897 Wasp alle
21	190	68.1	204	AAW35691	Aaw35691 Vespid an
22	184	65.9	32	AAE28810	Aae28810 Vesputa v
23	180	64.5	31	AAW35648	Aaw35648 T cell pe
24	174	62.4	31	AAW35647	Aaw35647 T cell pe

ALIGNMENTS

RESULT 1
AAE28827
ID AAE28827 standard; peptide; 50 AA.
XX
AC AAE28827;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #14.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
N-PSDB; RAD46272.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide

99	29	54.7	297	6	US-10-878-556A-119	Sequence 119, App	172	29	54.7	306	7	US-11-002-387-50	Sequence 50, Appl
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101	29	54.7	297	7	US-11-188-298-2744	Sequence 2744, App	174	29	54.7	306	7	US-11-002-387-52	Sequence 52, Appl
102	29	54.7	297	7	US-11-188-298-4525	Sequence 4525, App	175	29	54.7	306	7	US-11-002-387-53	Sequence 53, Appl
103	29	54.7	305	7	US-11-187-687-9	Sequence 9, Appl	176	29	54.7	306	7	US-11-002-387-54	Sequence 54, Appl
104	29	54.7	305	7	US-11-187-687-10	Sequence 10, Appl	177	29	54.7	306	7	US-11-002-387-55	Sequence 55, Appl
105	29	54.7	305	7	US-11-187-687-11	Sequence 11, Appl	178	29	54.7	306	7	US-11-002-387-56	Sequence 56, Appl
106	29	54.7	306	6	US-10-530-421-18	Sequence 18, Appl	179	29	54.7	306	7	US-11-002-387-57	Sequence 57, Appl
107	29	54.7	306	6	US-10-530-421-19	Sequence 19, Appl	180	29	54.7	306	7	US-11-002-387-58	Sequence 58, Appl
108	29	54.7	306	6	US-10-530-421-20	Sequence 20, Appl	181	29	54.7	306	7	US-11-002-387-59	Sequence 59, Appl
109	29	54.7	306	7	US-11-017-550-35	Sequence 35, Appl	182	29	54.7	306	7	US-11-002-387-60	Sequence 60, Appl
110	29	54.7	306	7	US-11-017-550-37	Sequence 37, Appl	183	29	54.7	306	7	US-11-002-387-61	Sequence 61, Appl
111	29	54.7	306	7	US-11-017-550-38	Sequence 38, Appl	184	29	54.7	306	7	US-11-002-387-62	Sequence 62, Appl
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115	29	54.7	306	7	US-11-017-550-42	Sequence 42, Appl	188	29	54.7	306	7	US-11-232-425-4	Sequence 4, Appl
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122	29	54.7	306	7	US-11-017-550-49	Sequence 49, Appl	195	29	54.7	306	7	US-11-232-425-18	Sequence 18, Appl
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126	29	54.7	306	7	US-11-017-550-53	Sequence 53, Appl	199	29	54.7	306	7	US-11-232-425-24	Sequence 24, Appl
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129	29	54.7	306	7	US-11-017-550-56	Sequence 56, Appl	202	29	54.7	329	7	US-11-188-298-1902	Sequence 1902, App
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132	29	54.7	306	7	US-11-017-550-59	Sequence 59, Appl	205	29	54.7	380	7	US-11-096-568A-3310	Sequence 3310, App
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135	29	54.7	306	7	US-11-017-550-62	Sequence 62, Appl	208	29	54.7	394	7	US-11-079-463-8871	Sequence 8871, App
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151	29	54.7	306	7	US-11-187-687-14	Sequence 14, Appl	224	29	54.7	3256	7	US-11-124-367A-432	Sequence 432, App
152	29	54.7	306	7	US-11-187-687-15	Sequence 15, Appl	225	29	54.7	3475	7	US-11-087-099-10885	Sequence 10885, A
153	29	54.7	306	7	US-11-187-687-16	Sequence 16, Appl	226	29	54.7	3475	6	US-10-467-657-2582	Sequence 2582, App
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155	29	54.7	306	7	US-11-187-687-18	Sequence 18, Appl	228	28	52.8	86	6	US-10-475-075-460	Sequence 175, App
156	29	54.7	306	7	US-11-187-687-19	Sequence 19, Appl	229	28	52.8	86	6	US-10-475-075-460	Sequence 460, App
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164	29	54.7	306	7	US-11-002-387-42	Sequence 42, Appl	237	28	52.8	200	7	US-11-087-099-3495	Sequence 3495, App
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168	29	54.7	306	7	US-11-002-387-46	Sequence 46, Appl	241	28	52.8	231	7	US-11-188-298-6620	Sequence 6620, App
169	29	54.7	306	7	US-11-002-387-47	Sequence 47, Appl	242	28	52.8	231	7	US-11-188-298-21886	Sequence 21886, A
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:28:47 ; Search time 9.16667 Seconds
(without alignments)
46.352 Million cell updates/sec

Title: US-10-091-135-13

Perfect score: 53

Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	36	67.9	244	7	US-11-156-084-218
6	35	66.0	749	7	US-11-079-463-5493
7	35	66.0	4868	7	US-11-044-111-24
8	34	64.2	215	6	US-10-793-626-828
9	34	64.2	407	7	US-11-079-463-8587
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13	33	62.3	465	7	US-11-156-084-101
14	33	62.3	2314	7	US-11-097-728-2
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19	32	60.4	218	7	US-11-096-568A-15081
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22	32	60.4	337	7	US-11-096-568A-10716
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75	30	56.6	554	7	US-11-096-568A-28079
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:24:04 ; Search time 13.9583 Seconds

(without alignments)
59.230 Million cell updates/sec

Title: US-10-091-135-13

Perfect score: 53

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Scoring table: BLOSUM62

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	47	88.7	204	2	US-09-130-287-2
6	47	88.7	227	2	US-09-541-759-6
7	44	83.0	354	2	US-09-198-452A-317
8	44	83.0	354	2	US-09-438-185A-305
9	39	73.6	950	2	US-09-248-796A-15047
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13	36	67.9	3696	2	US-09-134-001C-5080
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105	35	66.0	457	2	Q81BR4_PLAF7	Q81BR4 plasmodium	178	34	64.2	398	1	HRCA_CHLPN	Q92850 chlamydia p
106	35	66.0	482	2	Q61G01_CAEBR	Q61G01 caenorhabdi	179	34	64.2	404	2	Q64RQ0_BACFR	Q92850 bacteroides
107	35	66.0	485	2	Q9XVK0_CAEBL	Q9XVK0 caenorhabdi	180	34	64.2	414	2	Q7Q6H1_ANOGA	Q7Q6H1 anopheles g
108	35	66.0	492	2	Q4H3K6_CAMLA	Q4H3K6 campylobact	181	34	64.2	416	2	Q9C2D6_NEUCR	Q9C2D6 neurospora
109	35	66.0	496	2	Q4H104_GIBZE	Q4H104 gibberella	182	34	64.2	432	2	Q41BJ6_GIBZE	Q41BJ6 gibberella
110	35	66.0	502	1	PTL_LISIN	PTL_LISIN listeria in	183	34	64.2	443	2	Q5CUN2_CRYPV	Q5CUN2 cryptospori
111	35	66.0	512	1	PTL_LISNO	PTL_LISNO listeria in	184	34	64.2	443	2	Q5CPC4_CRYHO	Q5CPC4 cryptospori
112	35	66.0	572	2	Q72IG3_LISMF	Q72IG3 listeria mo	185	34	64.2	448	2	Q81JC4_PLAF7	Q81JC4 plasmodium
113	35	66.0	578	2	Q81S24_PLAF7	Q81S24 listeria mo	186	34	64.2	484	2	Q9QXX8_MOUSE	Q9QXX8 m nuclear f
114	35	66.0	599	1	FARE_BORBU	FARE_BORBU borrelia bu	187	34	64.2	485	1	RNF8_HUMAN	Q76064 homo sapien
115	35	66.0	599	2	Q662X6_BORCA	Q662X6 borrelia ga	188	34	64.2	485	2	Q53H16_HUMAN	Q53H16 homo sapien
116	35	66.0	630	2	Q8SQV0_ENCCU	Q8SQV0 encaphalito	189	34	64.2	485	2	Q5NKW5_HUMAN	Q5NKW5 homo sapien
117	35	66.0	742	2	Q5LCK8_BACFN	Q5LCK8 bacteroides	190	34	64.2	486	2	Q5R412_PONPY	Q5R412 pongo pygma
118	35	66.0	742	2	Q64TQ7_BACFR	Q64TQ7 bacteroides	191	34	64.2	487	2	Q52SA5_ORYSA	Q52SA5 oryza sativ
119	35	66.0	750	2	Q91D04_9VIRU	Q91D04 torque teno	192	34	64.2	488	1	RNF8_MOUSE	Q8VCS6 mus musculu
120	35	66.0	859	2	Q4YQV1_PLABE	Q4YQV1 mycoplasma	193	34	64.2	488	2	Q4FJV7_MOUSE	Q4FJV7 mus musculu
121	35	66.0	897	2	Q98QG9_MYCPU	Q98QG9 mycoplasma	194	34	64.2	511	2	Q4YUD4_PLABE	Q4YUD4 plasmodium
122	35	66.0	899	2	Q4YXB5_PLABE	Q4YXB5 plasmodium	195	34	64.2	511	2	Q4YVZ6_PLABE	Q4YVZ6 plasmodium
123	35	66.0	906	2	Q7RQF1_PLAYO	Q7RQF1 plasmodium	196	34	64.2	552	2	Q8VZC8_ARATH	Q8VZC8 arabidopsis
124	35	66.0	911	2	Q7RQJ2_PLAYO	Q7RQJ2 plasmodium	197	34	64.2	552	2	Q97046_HALRO	Q97046 halocynthia
125	35	66.0	962	2	Q6BGL0_PARTE	Q6BGL0 paramecium	198	34	64.2	565	2	Q72W94_LEPIC	Q72W94 leptospira
126	35	66.0	982	2	Q7BJR4_ANOGA	Q7BJR4 anopheles g	199	34	64.2	565	2	Q8F9Y8_LEPIN	Q8F9Y8 leptospira
127	35	66.0	1033	2	Q81BB8_PLAF7	Q81BB8 plasmodium	200	34	64.2	568	2	Q7RMU3_PLAYO	Q7RMU3 plasmodium
128	35	66.0	1228	2	Q9U4H2_DROME	Q9U4H2 drosophila	201	34	64.2	575	2	Q54FM9_DICDI	Q54FM9 dictyosteli
129	35	66.0	1268	2	Q5CVS0_CRYPV	Q5CVS0 cryptospori	202	34	64.2	590	2	Q4YIT7_PLABE	Q4YIT7 plasmodium
130	35	66.0	1268	2	Q5CJQ8_CRYHO	Q5CJQ8 cryptospori	203	34	64.2	620	1	ORC2_YEAST	P32833 saccharomyc
131	35	66.0	1317	2	Q5CVF5_CRYPV	Q5CVF5 cryptospori	204	34	64.2	628	2	Q97243_PLAF7	Q97243 plasmodium
132	35	66.0	1318	2	Q5CHP5_CRYHO	Q5CHP5 cryptospori	205	34	64.2	643	2	Q54Y78_DICDI	Q54Y78 dictyosteli
133	35	66.0	1440	2	Q4RPR0_TETNG	Q4RPR0 tetraodon n	206	34	64.2	656	2	Q6KH15_MYCWO	Q6KH15 mycoplasma
134	35	66.0	1583	2	Q6DNE6_9CYAN	Q6DNE6 lyngbya maj	207	34	64.2	690	1	Y173_UREPA	Q9P9X0 ureaplasma
135	35	66.0	1698	2	Q9V815_DROME	Q9V815 drosophila	208	34	64.2	749	2	Q6A027_MOUSE	Q6A027 mus musculu
136	35	66.0	1701	2	Q9V816_DROME	Q9V816 drosophila	209	34	64.2	778	2	Q4YNZ9_PLABE	Q4YNZ9 plasmodium
137	35	66.0	1712	2	Q6FPM0_PLAF7	Q6FPM0 plasmodium	210	34	64.2	829	2	Q54DN9_DICDI	Q54DN9 dictyosteli
138	35	66.0	1781	2	Q7PDN3_PLAYO	Q7PDN3 plasmodium	211	34	64.2	847	2	Q4PFJ1_USTMA	Q4PFJ1 ustilago ma
139	35	66.0	1922	2	Q8MLH7_DROME	Q8MLH7 drosophila	212	34	64.2	907	2	Q54J31_DICDI	Q54J31 dictyosteli
140	35	66.0	1923	2	Q6ANF2_DROME	Q6ANF2 drosophila	213	34	64.2	908	2	Q6CML0_KULA	Q6CML0 kluyveromyc
141	35	66.0	4097	2	Q7RG07_PLAYO	Q7RG07 plasmodium	214	34	64.2	1040	2	Q4YNV3_PLABE	Q4YNV3 plasmodium
142	35	66.0	4869	2	Q90985_CHICK	Q90985 gallus gall	215	34	64.2	1243	2	Q4Z6H8_PLABE	Q4Z6H8 plasmodium
143	35	66.0	6118	2	Q81396_PLAF7	Q81396 plasmodium	216	34	64.2	1370	2	Q8AB44_BACTN	Q8AB44 bacteroides
144	34	64.2	109	2	Q5JLE4_ORYSA	Q5JLE4 oryza sativ	217	34	64.2	1481	2	Q81BB3_PLAF7	Q81BB3 plasmodium
145	34	64.2	121	1	RL7A_THEAC	RL7A thermoplasm	218	34	64.2	2779	2	Q81LH0_PLAF7	Q81LH0 plasmodium
146	34	64.2	121	1	RL7A_THEVO	RL7A thermoplasm	219	34	64.2	3394	2	Q77384_PLAF7	Q77384 plasmodium
147	34	64.2	138	2	Q5WHE0_BACSK	Q5WHE0 bacillus ci	220	34	64.2	4507	2	Q7RFG7_PLAYO	Q7RFG7 plasmodium
148	34	64.2	152	2	Q5JF25_PYRKO	Q5JF25 pyrococcus	221	34	64.2	10578	2	Q81SF5_CABEL	Q81SF5 caenorhabdi
149	34	64.2	173	1	CD3D_MOUSE	P04235 mus musculu	222	34	64.2	18519	2	Q81SF6_CABEL	Q81SF6 caenorhabdi
150	34	64.2	173	1	CD3D_RAT	P19377 rattus norv	223	34	64.2	18534	2	Q81SF7_CABEL	Q81SF7 caenorhabdi
151	34	64.2	173	1	Q6P5F1_MOUSE	Q6P5F1 mus musculu	224	33	63.2	377	2	Q9WHG3_HPV18	Q9WHG3 human papil
152	34	64.2	191	2	P70895_BORCA	P70895 borrelia ga	225	33	62.3	59	2	Q54JZ5_DICDI	Q54JZ5 dictyosteli
153	34	64.2	192	2	Q9XGJ9_GNEGN	Q9XGJ9 gnetum gnet	226	33	62.3	61	2	Q5JTS3_WOLTR	Q5JTS3 wolbachia s
154	34	64.2	201	2	Q7QM18_ANOGA	Q7QM18 anopheles g	227	33	62.3	78	2	Q5ZSE4_LIEGPH	P59527 buchnera ap
155	34	64.2	203	2	Q4L9L1_STAHI	Q4L9L1 staphylococ	228	33	62.3	109	1	THIO_BUCBP	Q5284 legionella
156	34	64.2	215	2	Q5HRH5_STAEP	Q5HRH5 staphylococ	229	33	62.3	113	2	Q4Z5W7_PLABE	Q4Z5W7 plasmodium
157	34	64.2	233	2	Q8CQ68_STAEP	Q8CQ68 staphylococ	230	33	62.3	116	2	Q823C0_CHLCV	Q823C0 chlamydophi
158	34	64.2	233	2	Q7RR04_PLAYO	Q7RR04 plasmodium	231	33	62.3	125	2	Q515Y8_ENTHI	Q515Y8 entamoeba h
159	34	64.2	233	2	Q4YFA0_PLABE	Q4YFA0 plasmodium	232	33	62.3	126	2	Q8SR06_ENCCU	Q8SR06 encaphalito
160	34	64.2	245	2	Q4Y888_PLACH	Q4Y888 plasmodium	233	33	62.3	141	2	Q8GCI4_BACCE	Q8GCI4 bacillus ce
161	34	64.2	246	2	Q7TU63_PROMP	Q7TU63 prochloroco	234	33	62.3	145	2	Q64Q27_BACFR	Q64Q27 bacteroides
162	34	64.2	249	2	Q9CV69_MOUSE	Q9CV69 mus musculu	235	33	62.3	148	2	Q4X123_PLACH	Q4X123 plasmodium
163	34	64.2	268	2	Q5CXU9_CRYPV	Q5CXU9 cryptospori	236	33	62.3	148	2	Q8ETE0_OCEIH	Q8ETE0 oceanobacil
164	34	64.2	295	2	Q9USC1_CAEBL	Q9USC1 caenorhabdi	237	33	62.3	149	2	Q84SB9_ORYSA	Q84SB9 oryza sativ
165	34	64.2	296	2	Q96253_SULTO	Q96253 sulfolobus	238	33	62.3	162	2	Q6MTI2_MYCMS	Q6MTI2 mycoplasma
166	34	64.2	309	2	Q7RJL1_TETNG	Q7RJL1 tetraodon n	239	33	62.3	168	2	Q5A431_CANAL	Q5A431 candida alb
167	34	64.2	310	2	Q7R4N4_GIALA	Q7R4N4 giardia lam	240	33	62.3	168	2	Q5DHK4_SCHJA	Q5DHK4 schistosoma
168	34	64.2	345	2	Q4YQT9_PLABE	Q4YQT9 plasmodium	241	33	62.3	170	2	Q8RAD9_THETN	Q8RAD9 thermonaer
169	34	64.2	367	2	Q4YU99_PLABE	Q4YU99 plasmodium	242	33	62.3	183	2	Q84WJ5_BACFR	Q84WJ5 bacteroides
170	34	64.2	370	2	Q9K5S4_BACHD	Q9K5S4 bacillus ha	243	33	62.3	189	2	Q58WX6_ORENI	Q58WX6 oreochromis
171	34	64.2	377	2	Q9LNU7_ARATH	Q9LNU7 arabidopsis	244	33	62.3	209	2	Q8RRR7_HELPY	Q8RRR7 helicobacte
172	34	64.2	378	2	Q9HJF4_THEAC	Q9HJF4 thermoplasm	245	33	62.3	209	2	Q8RRS2_HELPY	Q8RRS2 helicobacte
173	34	64.2	386	1	HRCA_CHLAB	HRCA chlamydophi	246	33	62.3	214	2	Q8RRR6_HELPY	Q8RRR6 helicobacte
174	34	64.2	386	1	HRCA_CHLCV	HRCA chlamydophi	247	33	62.3	214	2	Q8RRR8_HELPY	Q8RRR8 helicobacte
175	34	64.2	391	2	Q5LBA3_BACFN	Q5LBA3 bacteroides	248	33	62.3	228	2	Q6ONC2_CAEBR	Q6ONC2 caenorhabdi
176	34	64.2	392	1	HRCA_CHLMU	P54306 chlamydia m	249	33	62.3	231	2	Q4XNG9_PLACH	Q4XNG9 plasmodium
177	34	64.2	392	1	HRCA_CHLTR	P36426 chlamydia t	250	33	62.3	241	2	Q6MKV7_BDEBA	Q6MKV7 bdellovibri

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 105.417 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-13
Perfect score: 53
Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	92.5	204	1 VA5_VESFL	P35783 vespula fla
2	49	92.5	204	1 VA5_VESMC	P35760 vespula mac
3	47	88.7	227	1 VA5_VESVU	Q05110 vespula vul
4	46	86.8	204	1 VA5_VESGE	P35784 vespula ger
5	46	86.8	204	1 VA5_VESPE	P35785 vespula pen
6	44	83.0	346	2 Q9K265 CHLPN	Q9K265 chlamydia p
7	44	83.0	346	2 Q928N5 CHLPN	Q928N5 chlamydia p
8	41	77.4	90	2 Q6TKM6 9MOLU	Q6TKM6 beet leafh
9	41	77.4	90	2 Q6TKM5 9MOLU	Q6TKM5 beet leafh
10	41	77.4	416	2 Q81366 PLAF7	Q81366 plasmodium
11	40	75.5	385	2 Q4MIF9 BACCE	Q4MIF9 bacillus ce
12	40	75.5	838	2 Q75G12 LEPIIC	Q75G12 leptospira
13	40	75.5	3165	2 Q81JL8 PLAF7	Q81JL8 plasmodium
14	39	73.6	123	2 Q4MHP6 BACCE	Q4MHP6 bacillus ce
15	39	73.6	245	2 Q81DD1_BACCR	Q81DD1 bacillus ce
16	39	73.6	246	2 Q81HL8_BACCH	Q81HL8 bacillus th
17	39	73.6	248	2 Q737X3_BACCI	Q737X3 bacillus ce
18	39	73.6	248	2 Q63B91_BACCC	Q63B91 bacillus ce
19	39	73.6	518	2 Q5TVD2 ANOGA	Q5TVD2 anopheles g
20	39	73.6	1235	2 Q5A7S2 CANAL	Q5A7S2 candida alb
21	38	71.7	343	2 Q5L613_CHLAB	Q5L613 chlamydia
22	38	71.7	547	2 Q8MYK6_9BILA	Q8MYK6 priapulus c
23	38	71.7	1386	2 Q54AS8 DICTDI	Q54AS8 dictyosteli
24	38	71.7	1422	2 Q54VD1_DICTDI	Q54VD1 dictyosteli
25	38	71.7	1437	2 Q9GQ51_DICDI	Q9GQ51 dictyosteli
26	37	69.8	158	2 Q5GHG3_CANOL	Q5GHG3 candida ole
27	37	69.8	158	2 Q4HFZ3_CAMCO	Q4HFZ3 campylobact
28	37	69.8	206	1 VA5_VESVI	P35787 vespula vid
29	37	69.8	299	2 Q7Q6J3 ANOGA	Q7Q6J3 anopheles g
30	37	69.8	416	2 Q96144 PLAF7	Q96144 plasmodium
31	37	69.8	454	2 Q9QY91_MOUSE	Q9QY91 mus musculus

32	37	69.8	674	2 Q9VC92 DROME	Q9VC92 drosophila
33	37	69.8	721	2 Q511V1_ENTHI	Q511V1 entamoeba h
34	37	69.8	791	2 Q5CY49_CRYPV	Q5CY49 cryptospori
35	37	69.8	791	2 Q5CN15_CRYHO	Q5CN15 cryptospori
36	37	69.8	838	2 Q8EY56_LEPIN	Q8EY56 leptospira
37	37	69.8	1615	2 Q6FK87_CANGA	Q6FK87 candida gla
38	37	69.8	1809	2 Q15892_TETTH	Q15892 tetrahymena
39	37	69.8	2627	2 Q4IQE1_GIBZE	Q4IQE1 gibberella
40	37	69.8	3009	2 Q7RGG0_PLAYO	Q7RGG0 plasmodium
41	37	69.8	4859	2 Q95201_MUSVI	Q95201 mustela vis
42	37	69.8	4859	2 Q7M2T9_9CARN	Q7M2T9 mustela sp.
43	37	69.8	4870	1 RYR3_HUMAN	Q15413 homo sapien
44	37	69.8	4872	2 Q9T533_RABIT	Q9T533 oryctolagus
45	36	67.9	109	2 Q8CV63_OCEIH	Q8CV63 oceanobacil
46	36	67.9	136	2 Q9WMN9_ANASP	Q9WMN9 anabaena sp
47	36	67.9	244	2 Q8Z078_ANASP	Q8Z078 anabaena sp
48	36	67.9	246	2 Q6HYL3_BACAN	Q6HYL3 bacillus an
49	36	67.9	248	2 Q810D6_BACAN	Q810D6 bacillus an
50	36	67.9	310	2 Q9BV59_HUMAN	Q9BV59 homo sapien
51	36	67.9	387	2 Q9PFY6_UREPA	Q9PFY6 ureaplasma
52	36	67.9	396	2 Q6NZC1_MOUSE	Q6NZC1 mus musculu
53	36	67.9	439	1 RNBP6_MOUSE	Q8BIV3 mus musculu
54	36	67.9	591	2 Q6K2L9_ORYSA	Q6K2L9 oryza sativ
55	36	67.9	798	2 Q7TN23_MOUSE	Q7TN23 mus musculu
56	36	67.9	964	2 Q6BG56_PARTE	Q6BG56 paramescium
57	36	67.9	995	2 Q54PU7_DICDI	Q54PU7 dictyosteli
58	36	67.9	1084	2 Q4R8T7_MACFA	Q4R8T7 macaca faec
59	36	67.9	1094	2 Q804V4_XENLA	Q804V4 xenopus lae
60	36	67.9	1094	2 Q7ZT67_XENLA	Q7ZT67 xenopus lae
61	36	67.9	1097	1 IMB3_HUMAN	Q00410 homo sapien
62	36	67.9	1097	1 IMB3_MOUSE	Q8BKC5 mus musculu
63	36	67.9	1097	2 Q5T578_HUMAN	Q5T578 homo sapien
64	36	67.9	1098	2 Q68FK3_XENLA	Q68FK3 xenopus lae
65	36	67.9	1105	1 RNBP6_HUMAN	Q60518 homo sapien
66	36	67.9	1105	2 Q5T7X4_HUMAN	Q5T7X4 homo sapien
67	36	67.9	1107	2 Q7ZT18_XENLA	Q7ZT18 xenopus lae
68	36	67.9	1115	2 Q86XC7_HUMAN	Q86XC7 homo sapien
69	36	67.9	1204	2 Q4Y6X5_PLACH	Q4Y6X5 plasmodium
70	36	67.9	1284	2 Q61VN1_CAEBR	Q61VN1 caenorhabdi
71	36	67.9	2282	2 Q9NK56_DROME	Q9NK56 drosophila
72	36	67.9	2501	2 Q4UIN5_THEAN	Q4UIN5 theileria a
73	36	67.9	2668	2 Q8IE42_PLAF7	Q8IE42 plasmodium
74	36	67.9	3692	2 Q5HNF3_STAEQ	Q5HNF3 staphylococ
75	36	67.9	3692	2 Q8CNU9_STAEQ	Q8CNU9 staphylococ
76	35	66.0	85	2 Q4YD72_PLABE	Q4YD72 plasmodium
77	35	66.0	133	2 Q4MMJ5_BACCE	Q4MMJ5 bacillus ce
78	35	66.0	147	2 Q8YMC1_ANASP	Q8YMC1 anabaena sp
79	35	66.0	148	2 Q6HK12_BACCH	Q6HK12 bacillus th
80	35	66.0	148	2 Q81EM1_BACCR	Q81EM1 bacillus ce
81	35	66.0	148	2 Q739V7_BACCI	Q739V7 bacillus ce
82	35	66.0	148	2 Q81RT9_BACAN	Q81RT9 bacillus an
83	35	66.0	148	2 Q63CK7_BACCC	Q63CK7 bacillus ce
84	35	66.0	185	2 Q694P4_LISMO	Q694P4 listeria mo
85	35	66.0	187	2 Q7KMU7_DICDI	Q7KMU7 dictyosteli
86	35	66.0	229	2 Q4Y010_PLACH	Q4Y010 plasmodium
87	35	66.0	235	2 Q559J3_DICDI	Q559J3 dictyosteli
88	35	66.0	252	2 Q7LV9_CLOAB	Q7LV9 clostridium
89	35	66.0	258	2 Q4SP53_TETNG	Q4SP53 tetraodon n
90	35	66.0	343	2 Q5VR28_ORYSA	Q5VR28 oryza sativ
91	35	66.0	367	2 Q81371_PLAF7	Q81371 plasmodium
92	35	66.0	401	2 Q4MWA7_BACCE	Q4MWA7 bacillus ce
93	35	66.0	401	2 Q81UF1_BACAN	Q81UF1 bacillus an
94	35	66.0	402	2 Q812N2_BACAN	Q812N2 bacillus an
95	35	66.0	424	2 Q4MG21_BACCE	Q4MG21 bacillus ce
96	35	66.0	424	2 Q6HF27_BACCH	Q6HF27 bacillus th
97	35	66.0	424	2 Q732T8_BACCI	Q732T8 bacillus ce
98	35	66.0	424	2 Q81A08_BACCR	Q81A08 bacillus an
99	35	66.0	424	2 Q81WP6_BACAN	Q81WP6 bacillus an
100	35	66.0	424	2 Q636N8_BACCC	Q636N8 bacillus ce
101	35	66.0	425	2 Q7X275_9RHIZ	Q7X275 bartonella
102	35	66.0	426	2 Q6FYK4_BAROU	Q6FYK4 bartonella
103	35	66.0	433	2 Q7RTF2_PLABO	Q7RTF2 plasmodium
104	35	66.0	455	2 Q4YXU4_PLABE	Q4YXU4 plasmodium

103	31	58.5	110	2	S22459	hypothetical 12.3K	176	31	58.5	509	2	I45713	Dpp receptor TKV,
104	31	58.5	132	2	S57883	T-cell receptor be	177	31	58.5	519	2	C90085	hypothetical prote
105	31	58.5	134	2	T30680	hypothetical prote	178	31	58.5	519	2	C86160	hypothetical prote
106	31	58.5	154	2	JH0248	guanine nucleotide	179	31	58.5	523	2	D86492	hypothetical prote
107	31	58.5	172	2	G90319	hypothetical prote	180	31	58.5	523	2	D72130	hypothetical prote
108	31	58.5	189	2	AF1233	signal peptidase I	181	31	58.5	527	2	A54985	BMP receptor precu
109	31	58.5	198	2	AD1596	signal peptidase I	182	31	58.5	532	2	I37163	ALK-3 - human
110	31	58.5	207	2	S07130	casein B precursor	183	31	58.5	532	2	JC2387	bone morphogenetic
111	31	58.5	205	2	D44583	venom allergen ant	184	31	58.5	532	2	A56238	bone morphogenetic
112	31	58.5	207	2	B85649	hypothetical prote	185	31	58.5	532	2	A56238	zinc finger protei
113	31	58.5	207	2	A99789	hypothetical prote	186	31	58.5	540	2	B57785	epidermal keratin
114	31	58.5	209	2	F90324	hypothetical prote	187	31	58.5	553	2	I59009	sulfite reductase
115	31	58.5	213	2	AG2785	hypothetical prote	188	31	58.5	553	2	AH2472	hypothetical prote
116	31	58.5	216	2	C75102	hypothetical prote	189	31	58.5	596	2	B96834	serine/threonine k
117	31	58.5	217	2	A97565	hypothetical prote	190	31	58.5	601	2	A55921	gsp-binding protei
118	31	58.5	233	2	H90294	hypothetical prote	191	31	58.5	642	2	T40600	hypothetical prote
119	31	58.5	237	2	C84065	transcription regu	192	31	58.5	648	2	D91000	unknown protein en
120	31	58.5	240	2	H72294	ribonuclease III -	193	31	58.5	655	2	F85845	Flu11.27 [importe
121	31	58.5	242	2	A81300	probable diaminopi	194	31	58.5	685	2	T32571	hypothetical prote
122	31	58.5	249	2	A41972	replication-associ	195	31	58.5	702	2	E35216	hypothetical prote
123	31	58.5	259	2	T24433	hypothetical prote	196	31	58.5	791	2	S05988	translation elonga
124	31	58.5	277	2	T31710	hypothetical prote	197	31	58.5	844	2	S05988	translation elonga
125	31	58.5	281	2	B90167	conserved hypothet	198	31	58.5	858	1	BFH2	translation elonga
126	31	58.5	284	2	AB1343	transcription regu	199	31	58.5	858	1	EFRT2	translation elonga
127	31	58.5	286	2	G65537	ribosomal protein	200	31	58.5	858	2	A25440	hypothetical prote
128	31	58.5	287	2	E95227	transcription regu	201	31	58.5	859	2	C90088	hypothetical prote
129	31	58.5	287	2	A99092	transcription acti	202	31	58.5	864	2	T31973	hypothetical prote
130	31	58.5	288	2	C86687	hypothetical prote	203	31	58.5	868	2	S65186	NI80 protein - ye
131	31	58.5	292	2	T33322	hypothetical prote	204	31	58.5	897	2	T21688	probable membrane
132	31	58.5	301	2	AF1024	probable membrane	205	31	58.5	939	2	S55985	hypothetical prote
133	31	58.5	311	2	B85530	thioredoxin reduct	206	31	58.5	1111	2	G96693	different proteins
134	31	58.5	324	2	T24758	thioredoxin reduct	207	31	58.5	1136	2	AH1227	probable RNA-dirc
135	31	58.5	325	2	H71869	hypothetical prote	208	31	58.5	1215	2	T11660	hypothetical prote
136	31	58.5	336	2	T44605	F420-dependent glu	209	31	58.5	1220	2	T32916	hypothetical prote
137	31	58.5	337	2	T18431	hypothetical prote	210	31	58.5	1250	2	E81339	probable restricti
138	31	58.5	340	2	T02120	hypothetical prote	211	31	58.5	1250	2	A86289	probable ABC trans
139	31	58.5	341	2	E90128	hypothetical prote	212	31	58.5	1568	2	T09074	senaphorin recepto
140	31	58.5	342	2	AC1507	hypothetical prote	213	31	58.5	1568	2	B86128	hypothetical prote
141	31	58.5	357	2	H90357	transposase ISCI22	214	31	58.5	1644	2	B86128	hypothetical prote
142	31	58.5	357	2	B90360	transposase ISCI22	215	31	58.5	1644	2	B86128	hypothetical prote
143	31	58.5	362	2	T02522	origin recognition	216	31	58.5	1650	2	T18444	hypothetical prote
144	31	58.5	363	2	G71950	phosphonoacetate h	217	31	58.5	1846	2	T33079	probable heat shoc
145	31	58.5	369	2	A81303	branched-chain ami	218	31	58.5	1871	2	D36796	hypothetical prote
146	31	58.5	369	2	G81303	hypothetical prote	219	31	58.5	2206	2	G71611	hypothetical prote
147	31	58.5	372	2	AH2214	hypothetical prote	220	31	58.5	2685	2	T38755	genome polyprotein
148	31	58.5	379	2	T28211	hypothetical membr	221	31	58.5	2875	1	RRVUTW	hypothetical prote
149	31	58.5	394	2	B82931	diaminopimelate de	222	31	58.5	2911	2	T20566	genome polyprotein
150	31	58.5	405	2	B64556	diaminopimelate de	223	31	58.5	3054	1	GMBVEV	Erba kinase activa
151	31	58.5	405	2	F71950	hypothetical prote	224	30	56.6	57	2	PC4415	tyrosine kinase -
152	31	58.5	419	2	T18450	receptor protein k	225	30	56.6	60	2	S43515	hypothetical prote
153	31	58.5	440	2	A56693	hypothetical prote	226	30	56.6	100	2	H89851	hypothetical prote
154	31	58.5	445	2	S64418	hypothetical prote	227	30	56.6	107	2	S50516	hypothetical prote
155	31	58.5	448	2	F89950	glutamyl-tRNA redu	228	30	56.6	109	2	S77444	hypothetical prote
156	31	58.5	476	2	I80182	activin type I rec	229	30	56.6	147	2	C71145	transcription regu
157	31	58.5	479	2	S64587	activin type I rec	230	30	56.6	149	2	D83758	hypothetical prote
158	31	58.5	487	2	I80183	hypothetical prote	231	30	56.6	168	2	T16285	hypothetical prote
159	31	58.5	491	2	S73844	conserved hypothet	232	30	56.6	180	2	T16445	hypothetical prote
160	31	58.5	491	2	B81558	glucose-6-phosphat	233	30	56.6	182	2	A28508	T-cell surface gly
161	31	58.5	494	2	A89930	related to PRP9 pr	234	30	56.6	192	2	H70375	conserved hypothet
162	31	58.5	497	2	T48730	hypothetical prote	235	30	56.6	211	2	C64336	hypothetical prote
163	31	58.5	497	2	H70168	transforming growt	236	30	56.6	225	2	F97349	response regulator
164	31	58.5	499	2	JC2062	receptor protein k	237	30	56.6	233	2	A69331	conserved hypothet
165	31	58.5	502	2	A56683	activin receptor-l	238	30	56.6	236	2	F83520	phosphoribosylamin
166	31	58.5	502	2	AD0691	conserved hypothet	239	30	56.6	247	2	JG0016	epidermal cell dif
167	31	58.5	502	2	AD0691	serine/threonine k	240	30	56.6	251	2	B69816	hypothetical prote
168	31	58.5	502	2	JC2491	transforming growt	241	30	56.6	257	2	JU0403	hypothetical 28.1K
169	31	58.5	503	2	JC2061	activin receptor-l	242	30	56.6	282	2	A43084	vitellogenin 4 pre
170	31	58.5	503	2	A49432	type I serine-thre	243	30	56.6	284	2	C64527	M protein - Helico
171	31	58.5	505	2	I33417	activin A receptor	244	30	56.6	286	2	F82881	hypothetical prote
172	31	58.5	505	2	I38859	monooxygenase [imp	245	30	56.6	289	2	T06565	acetyl-CoA carboxy
173	31	58.5	506	2	G86509	monooxygenase - Ch	246	30	56.6	303	2	AB1198	antibiotic ABC tra
174	31	58.5	506	2	A72113		247	30	56.6	307	2	F87952	protein T36E3.4 [i
175	31	58.5	506	2	A72113		248	30	56.6	308	2	T11956	hypothetical prote
										312	4	A40473	RNA-directed RNA p

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 16.6667 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-13
Perfect score: 53
Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80.*

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	92.5	204	2 B37329	antigen 5 - easter
2	49	92.5	204	2 A44583	venom allergen ant
3	46	86.8	204	2 B44583	venom allergen ant
4	46	86.8	204	2 C44583	venom allergen ant
5	44	83.0	346	2 G72094	ct244 hypothetical
6	44	83.0	346	2 G86528	CT244 hypothetical
7	44	83.0	346	2 B81574	conserved hypothet
8	37	69.8	206	2 E44583	venom allergen ant
9	37	69.8	416	2 C71620	protein with Egl-1
10	37	69.8	4859	2 S74173	ryanodine receptor
11	37	69.8	4872	2 S27272	ryanodine receptor
12	36	67.9	244	2 A01834	isopentenyl transf
13	36	67.9	387	2 E82881	hypothetical prote
14	35	66.0	147	2 AE2432	hypothetical prote
15	35	66.0	252	2 F96954	protein, containin
16	35	66.0	485	2 T24115	hypothetical prote
17	35	66.0	572	2 AC1200	phosphotransferase
18	35	66.0	572	2 A11557	phosphotransferase
19	35	66.0	599	2 D70104	DNA topoisomerase
20	35	66.0	599	2 C90561	hypothetical prote
21	35	66.0	4869	2 S66572	ryanodine receptor
22	34	64.2	173	1 RWSMD2	T-cell surface gly
23	34	64.2	173	2 S10975	T-cell surface gly
24	34	64.2	370	2 F84151	response regulator
25	34	64.2	392	2 H71520	probable hth trans
26	34	64.2	392	2 F81676	heat shock gene re
27	34	64.2	398	2 A86553	HTH transcription
28	34	64.2	398	2 G72070	hth transcription
29	34	64.2	407	2 B81598	heat shock gene re

30	64.2	620	2	S38994	origin recognition
31	64.2	630	2	H82823	conserved hypothet
32	64.2	3394	2	T18501	hypothetical prote
33	62.3	254	2	S55136	probable dehydro
34	62.3	279	2	S52582	prephenate cyclase
35	62.3	297	2	S66102	protein secretion
36	62.3	453	2	B49022	tryptophanase (EC
37	62.3	454	2	B84699	hypothetical prote
38	62.3	478	2	T05423	probable glucosylt
39	62.3	505	1	S13744	glucose-6-phosphat
40	62.3	512	2	T14638	cytochrome P450 CY
41	62.3	596	2	G82874	conserved hypothet
42	62.3	636	2	I61718	neu differentiation
43	62.3	637	2	C43273	heregulin precursor
44	62.3	701	2	S35313	TIP1 protein - yea
45	62.3	779	2	T20654	hypothetical prote
46	62.3	1082	2	T41988	hypothetical prote
47	62.3	1186	2	C64588	cag pathogenicity
48	62.3	1291	2	S02021	micropia polyprote
49	62.3	1302	1	RRXRBT	RNA-directed RNA p
50	62.3	2314	1	A46151	protein-tyrosine-p
51	62.3	2925	2	T00133	RNA-directed RNA p
52	60.4	76	2	T42309	hypothetical prote
53	60.4	78	2	H70020	hypothetical prote
54	60.4	82	1	CCAV5	cytochrome c551 -
55	60.4	107	2	F86869	hypothetical prote
56	60.4	149	2	D69666	nucleoside-diphosp
57	60.4	220	2	S45927	probable finger pr
58	60.4	274	2	T12791	hypothetical prote
59	60.4	287	2	E95313	cytochrome-c oxida
60	60.4	297	2	F64206	lipopolysaccharide
61	60.4	298	2	G64465	modification methy
62	60.4	326	2	AB1431	AraC-type regulato
63	60.4	326	2	AH1804	AraC-type regulato
64	60.4	332	2	T24312	hypothetical prote
65	60.4	334	2	F89008	protein W08A12.4 [
66	60.4	371	2	T44297	response regulator
67	60.4	393	2	AD2376	transcription regu
68	60.4	448	2	C97757	hypothetical prote
69	60.4	476	2	I37136	adenylate cyclase
70	60.4	478	2	JQ2034	RNA-directed RNA p
71	60.4	489	2	H64224	hypothetical prote
72	60.4	492	2	T21797	hypothetical prote
73	60.4	503	2	C84595	similar to pEARL1
74	60.4	504	2	D86432	hypothetical prote
75	60.4	540	2	S65321	tRNA-pseudouridine
76	60.4	544	2	S65321	hypothetical prote
77	60.4	548	2	T18761	hypothetical prote
78	60.4	604	2	S15794	lin-9 protein - Ca
79	60.4	608	2	T18437	hypothetical prote
80	60.4	610	2	A88542	hypothetical prote
81	60.4	634	2	G90779	hypothetical prote
82	60.4	635	2	S75668	DNA primase (EC 2.
83	60.4	645	2	A85641	hypothetical prote
84	60.4	689	2	F81286	probable polysacch
85	60.4	723	2	H85092	hypothetical prote
86	60.4	751	2	T21967	hypothetical prote
87	60.4	758	2	C96749	hypothetical prote
88	60.4	844	2	S47274	membrane alanyl am
89	60.4	844	2	JC4054	membrane alanyl am
90	60.4	848	2	G90128	elongation factor
91	60.4	971	2	C82880	conserved hypothet
92	60.4	1047	2	T34946	probable isoleucyl
93	60.4	1090	2	A41541	adenylate cyclase
94	60.4	1092	2	T18354	adhesin - Mycoplas
95	60.4	1099	2	T18357	mup1 protein - Myc
96	60.4	1102	2	S65235	probable membrane
97	60.4	1108	2	T18353	reverse gyrase - A
98	60.4	1171	2	G70399	gene u-shaped prot
99	60.4	1191	2	T13850	exodeoxyribonuclea
100	60.4	1211	2	D64116	valine-tRNA ligase
101	60.4	1296	2	S55511	hypothetical prote
102	58.5	105	2	H97704	

98	33	62.3	19	2	AAR56635	Aar56635 Tyrosine	171	33	62.3	631	5	ABJ00060	Abj00060 Human neu
99	33	62.3	63	3	AAB36703	Aab36703 EGF-like	172	33	62.3	636	2	AAR68576	Aar68576 Rat NDF e
100	33	62.3	63	3	AAB36707	Aab36707 EGF-like	173	33	62.3	636	2	AAR68573	Aar68573 Rat NDF e
101	33	62.3	119	4	AAG67932	Aag67932 Human NRG	174	33	62.3	637	2	AAR29573	Aar29573 Human her
102	33	62.3	119	4	AAG67970	Aag67970 Human NRG	175	33	62.3	637	2	AAY06636	Aay06636 Herugelin
103	33	62.3	119	5	ABJ00042	Abj00042 Human neu	176	33	62.3	637	3	AAY71173	Aay71173 Human Her
104	33	62.3	119	5	ABJ00080	Abj00080 Human neu	177	33	62.3	637	4	AAG67912	Aag67912 Human NRG
105	33	62.3	119	7	ADW70334	Adw70334 Human neu	178	33	62.3	637	4	AAG67950	Aag67950 Human NRG
106	33	62.3	119	8	ADH77519	Adh77519 Human neu	179	33	62.3	637	4	AAG67950	Aag67950 Human NRG
107	33	62.3	129	4	AAG67931	Aag67931 Human NRG	180	33	62.3	637	4	ADW70304	Adw70304 Human neu
108	33	62.3	129	4	AAG67969	Aag67969 Human NRG	181	33	62.3	843	8	ADT60678	Adt60678 Plant pol
109	33	62.3	129	5	ABJ00041	Abj00041 Human neu	182	33	62.3	1116	4	ABB62378	Abb62378 Drosophil
110	33	62.3	129	5	ABJ00079	Abj00079 Human neu	183	33	62.3	1186	8	ADU05584	Adu05584 H. pylori
111	33	62.3	129	5	ABJ00041	Abj00041 Human neu	184	33	62.3	2308	4	AAR57902	Aar57902 Human RPI
112	33	62.3	129	7	ADW70323	Adw70323 Human neu	185	33	62.3	2308	4	AAB59586	Aab59586 Human rep
113	33	62.3	129	8	ADH77518	Adh77518 Human neu	186	33	62.3	2308	4	ABG72433	Abg72433 Receptor
114	33	62.3	167	9	ADY28391	Ady28391 Novel Erb	187	33	62.3	2308	6	ABR58521	AbR58521 Human pro
115	33	62.3	192	4	AAG67900	Aag67900 Human neu	188	33	62.3	2314	6	ABU56692	Abu56692 Lung can
116	33	62.3	192	4	AAG67938	Aag67938 Human neu	189	33	62.3	2314	6	ABU56692	Abu56692 Lung can
117	33	62.3	192	5	ABJ00010	Abj00010 Human neu	190	33	62.3	2314	6	ABU56692	Abu56692 Lung can
118	33	62.3	192	5	ABJ00048	Abj00048 Human neu	191	33	62.3	2314	7	ADT62042	Adt62042 Human pro
119	33	62.3	192	7	ADW70292	Adw70292 Human neu	192	33	62.3	2314	7	ADT62042	Adt62042 Human pro
120	33	62.3	192	8	ADH77487	Adh77487 Human neu	193	33	62.3	2314	7	ADN39064	Adn39064 Cancer/an
121	33	62.3	253	3	AAB24132	Aab24132 Plasmodiu	194	33	62.3	2314	8	ADJ75597	Adj75597 Marker ge
122	33	62.3	276	2	AAR68566	Aar68566 Human pro	195	33	62.3	2314	8	ADU06410	Adu06410 Novel bro
123	33	62.3	282	4	ABR66530	AbR66530 Drosophil	196	33	62.3	2314	9	ADV70177	Adv70177 Tumor-agg
124	33	62.3	284	5	ABU51953	Abu51953 Helicobac	197	33	62.3	2314	9	AEA00158	Aea00158 Human TAR
125	33	62.3	298	2	AAR68575	Aar68575 Rat NDF e	198	33	62.3	2314	9	AEA04969	Aea04969 Protein t
126	33	62.3	300	2	AAW11503	Aaw11503 Humanised	199	33	62.3	2314	9	AEA04969	Aea04969 Protein t
127	33	62.3	300	2	AAW73218	Aaw73218 H22-HRG f	200	33	62.3	2314	9	AEA04969	Aea04969 Protein t
128	33	62.3	300	4	AAB61954	Aab61954 Amino aci	201	33	62.3	2315	6	ABU56687	Abu56687 Lung can
129	33	62.3	316	8	AAB85449	Aab85449 H22-HRG f	202	33	62.3	2315	6	ABU56687	Abu56687 Lung can
130	33	62.3	323	3	AAG21801	Aag21801 Arabidops	203	33	62.3	2315	6	ADN39942	Adn39942 Cancer/an
131	33	62.3	323	3	AAG40014	Aag40014 Arabidops	204	33	62.3	2315	6	ADN39942	Adn39942 Cancer/an
132	33	62.3	326	6	ABU44164	Abu44164 Protein e	205	32	60.4	15	8	ADP26430	Adp26430 Plasmodiu
133	33	62.3	335	3	AAG21800	Aag21800 Arabidops	206	32	60.4	46	3	ADP26430	Adp26430 Plasmodiu
134	33	62.3	335	3	AAG40013	Aag40013 Arabidops	207	32	60.4	61	8	ADP26430	Adp26430 Plasmodiu
135	33	62.3	348	4	ABR50156	AbR50156 Human tra	208	32	60.4	61	8	ADP26430	Adp26430 Plasmodiu
136	33	62.3	348	5	AAW48914	Aaw48914 Human tra	209	32	60.4	61	8	ADP26430	Adp26430 Plasmodiu
137	33	62.3	348	5	ABP64715	Abp64715 Human pro	210	32	60.4	61	8	ADP26430	Adp26430 Plasmodiu
138	33	62.3	356	5	ABU51625	Abu51625 Helicobac	211	32	60.4	71	5	ABP10949	Abp10949 Human ORF
139	33	62.3	374	3	AAG21799	Aag21799 Arabidops	212	32	60.4	96	2	AAV27352	Aav27352 Group B S
140	33	62.3	374	3	AAG40012	Aag40012 Arabidops	213	32	60.4	96	5	ADP28992	Adp28992 Streptoco
141	33	62.3	377	8	ADP98902	Adp98902 C. albica	214	32	60.4	96	5	ADP28992	Adp28992 Streptoco
142	33	62.3	378	4	ABR66800	AbR66800 Drosophil	215	32	60.4	96	8	ADV88777	Adv88777 Streptoco
143	33	62.3	379	5	ABU50882	Abu50882 Helicobac	216	32	60.4	96	8	ADV88777	Adv88777 Streptoco
144	33	62.3	389	5	ABU51383	Abu51383 Helicobac	217	32	60.4	98	6	ABR41634	AbR41634 Human DIT
145	33	62.3	420	2	AAR29575	Aar29575 Human her	218	32	60.4	105	6	ABR41634	AbR41634 Human DIT
146	33	62.3	420	2	AAY06638	Aay06638 Herugelin	219	32	60.4	107	5	ABR41634	AbR41634 Human DIT
147	33	62.3	420	2	AAV71175	Aav71175 Human her	220	32	60.4	110	5	ABP28503	Abp28503 Streptoco
148	33	62.3	420	4	AAU09890	Aau09890 Human her	221	32	60.4	144	7	ADP28503	Adp28503 Streptoco
149	33	62.3	420	5	ABU51367	Abu51367 Helicobac	222	32	60.4	149	8	ADP28503	Adp28503 Streptoco
150	33	62.3	422	5	ABU51614	Abu51614 Helicobac	223	32	60.4	212	4	ADP28503	Adp28503 Streptoco
151	33	62.3	438	7	ABM87032	Abm87032 Rice abio	224	32	60.4	245	5	ADP28503	Adp28503 Streptoco
152	33	62.3	454	3	ABR08439	AbR08439 Recombina	225	32	60.4	246	5	ADP28503	Adp28503 Streptoco
153	33	62.3	460	3	AAG40011	Aag40011 Arabidops	226	32	60.4	246	5	ADP28503	Adp28503 Streptoco
154	33	62.3	465	8	ADP43026	Adp43026 IPT-like	227	32	60.4	275	6	ADP28503	Adp28503 Streptoco
155	33	62.3	465	8	ADP43026	Adp43026 IPT-like	228	32	60.4	297	6	ADP28503	Adp28503 Streptoco
156	33	62.3	478	5	ABR93231	AbR93231 Herbicida	229	32	60.4	301	4	ABU70601	Abu70601 Bacillus
157	33	62.3	480	7	ABM90074	Abm90074 Rice abio	230	32	60.4	311	3	ABR45463	AbR45463 Human pan
158	33	62.3	481	3	AAG40009	Aag40009 Arabidops	231	32	60.4	326	5	ABR45463	AbR45463 Human pan
159	33	62.3	481	4	AAE07509	Aae07509 Arabidops	232	32	60.4	342	8	ADY04346	Ady04346 Plant pol
160	33	62.3	481	8	ADN72645	Adn72645 Thale cre	233	32	60.4	342	8	ADY04346	Ady04346 Plant pol
161	33	62.3	505	8	ADN19299	Adn19299 Bacterial	234	32	60.4	367	3	AAG32020	Aag32020 Arabidops
162	33	62.3	512	6	ADA48020	Ada48020 Rice prot	235	32	60.4	397	4	ABR63523	AbR63523 Drosophil
163	33	62.3	512	6	ADA48020	Ada48020 Rice prot	236	32	60.4	412	3	AAG50043	Aag50043 Arabidops
164	33	62.3	516	8	ADY13102	Ady13102 Plant ful	237	32	60.4	429	2	AAR94561	Aar94561 Human ade
165	33	62.3	536	8	ADT56220	Adt56220 Plant ful	238	32	60.4	434	2	AAR94561	Aar94561 Human ade
166	33	62.3	596	6	ABU48987	Abu48987 Protein e	239	32	60.4	457	3	AAR94561	Aar94561 Human ade
167	33	62.3	604	8	ADN26327	Adn26327 Bacterial	240	32	60.4	478	8	ADN17311	Adn17311 Beet cryp
168	33	62.3	623	7	ADC95099	Adc95099 E. faeciu	241	32	60.4	501	8	ADT50054	Adt50054 Oll-aegoc
169	33	62.3	629	7	ADH77499	Adh77499 Human neu	242	32	60.4	502	3	AAG50042	Aag50042 Arabidops
170	33	62.3	631	5	ABJ00022	Abj00022 Human neu	243	32	60.4	503	3	AAG32018	Aag32018 Arabidops

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 87.9167 Seconds
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49.977 Million cell updates/sec

Title: US-10-091-135-13

Perfect score: 53

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Scoring table: BLOSUM62

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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	53	100.0	49	5	Aae28814
3	53	100.0	204	2	Aay45217
4	53	100.0	204	5	Abg66977
5	53	100.0	204	5	Abg66983
6	53	100.0	204	5	Abg67052
7	53	100.0	204	5	Abg67104
8	53	100.0	204	5	Abg67103
9	53	100.0	204	5	Aae28820
10	53	100.0	209	4	Abm00031
11	49	92.5	204	2	Aaw35687
12	47	88.7	204	2	Aay25644
13	47	88.7	227	2	Aae13071
14	47	88.7	227	4	Adc34893
15	47	88.7	227	7	Adc34899
16	44	83.0	354	2	Aay34899
17	39	73.6	1235	8	Adp98882
18	38	71.7	604	3	Aab16602
19	37	69.8	206	2	Aay25648
20	37	69.8	206	7	Adc34897
21	37	69.8	416	3	Aab18185
22	37	69.8	674	4	Abp62357
23	37	69.8	1425	4	Abg23344
24	37	69.8	4771	4	Aau02939

25	37	69.8	4866	2	AAW77410	Human rya
26	37	69.8	4899	4	ABG12314	Novel hum
27	37	69.8	4899	7	ADF60293	Human con
28	37	69.8	4934	4	ABG23346	Novel hum
29	36	67.9	71	4	AAG75080	Human col
30	36	67.9	86	5	ABP42496	Human ova
31	36	67.9	135	3	AAB38300	Human sec
32	36	67.9	135	3	AAB38299	Human sec
33	36	67.9	135	3	AAB38305	Gene 35 h
34	36	67.9	135	3	AAB38306	Human sec
35	36	67.9	136	8	ADR43249	IPT-like
36	36	67.9	136	8	ADR43249	Bacterial
37	36	67.9	152	4	AAO02594	Human pol
38	36	67.9	244	8	ABU70525	IPT-like
39	36	67.9	310	6	ABU70525	Human adi
40	36	67.9	1097	6	AAO30432	Human kar
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42	36	67.9	1097	8	ADO19838	Human PRO
43	36	67.9	1097	8	ADQ18847	Human sof
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46	36	67.9	1105	4	ABG05389	Novel hum
47	36	67.9	1105	6	AAO30433	Human RAN
48	36	67.9	1105	8	ADP54967	Human PRO
49	36	67.9	1115	8	ADL13164	Human ste
50	36	67.9	1126	4	ABG30229	Novel hum
51	36	67.9	3692	6	ABU43311	Protein e
52	36	67.9	3692	8	ADS20647	S. epider
53	36	67.9	3696	5	ABP40235	Staphyloc
54	36	67.9	3696	8	ADS06647	Staphyloc
55	35	66.0	152	6	ADP09334	Alloioococ
56	35	66.0	427	8	ADT92052	Sugar bee
57	35	66.0	485	8	ADN23927	Bacterial
58	35	66.0	572	5	ABBA49227	Listeria
59	35	66.0	572	6	ABU32704	Protein e
60	35	66.0	798	3	AAB25551	Eucalyptu
61	35	66.0	1240	4	ABB61596	Drosophil
62	35	66.0	4544	8	ADP25443	Plasmodiu
63	34	64.2	20	2	AAR79995	ARH1 pept
64	34	64.2	26	3	AAV52320	Multisub
65	34	64.2	26	6	ABU08907	Mouse imm
66	34	64.2	26	7	ADH74786	Mouse imm
67	34	64.2	57	9	ABM96055	M. xanthu
68	34	64.2	109	8	ADT87653	Plant hom
69	34	64.2	215	4	AAG81867	S. epider
70	34	64.2	224	5	ABP40450	Staphyloc
71	34	64.2	224	8	ADS05989	Staphyloc
72	34	64.2	240	8	ADN73822	Plant ful
73	34	64.2	287	6	ADN73822	Alloioococ
74	34	64.2	302	8	ADN74187	Thale cre
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81	34	64.2	485	4	AAV95017	Human pro
82	34	64.2	485	7	ADJ58637	Human hea
83	34	64.2	517	8	ADJ58637	Plant ful
84	34	64.2	603	8	ADY04542	Plant ful
85	34	64.2	620	2	AAV77275	ORC2 subu
86	34	64.2	620	5	AAU82999	S. cerevi
87	34	64.2	620	6	ABR53643	Protein s
88	34	64.2	620	7	ADN64130	Disease t
89	34	64.2	620	8	ADN18789	Bacterial
90	34	64.2	645	8	ADN93364	Plant ful
91	34	64.2	749	8	ADN10498	Mouse pro
92	34	64.2	820	4	AAU35178	Enterococ
93	34	64.2	824	7	ADH87023	Enterococ
94	34	64.2	824	7	ADH87023	Enterococ
95	33	62.3	19	2	AAR56641	Tyrosine
96	33	62.3	19	2	AAR56636	Tyrosine
97	33	62.3	19	2	AAR56642	Tyrosine

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100	29	69.0	915	7	US-11-205-935-22	Sequence 22, Appl	173	28	66.7	852	7	US-11-050-804-6	Sequence 6, Appl
101	29	69.0	917	7	US-11-144-987-18	Sequence 18, Appl	174	28	66.7	875	7	US-11-087-099-7790	Sequence 7790, Ap
102	29	69.0	917	7	US-11-144-987-20	Sequence 20, Appl	175	28	66.7	875	7	US-11-188-298-18220	Sequence 18220, A
103	29	69.0	917	7	US-11-144-987-24	Sequence 24, Appl	176	28	66.7	885	7	US-11-072-512-2946	Sequence 2946, Ap
104	29	69.0	917	7	US-11-144-987-26	Sequence 26, Appl	177	28	66.7	885	7	US-10-517-939-258	Sequence 258, App
105	29	69.0	917	7	US-11-205-935-18	Sequence 18, Appl	178	28	66.7	1075	6	US-10-745-586-197	Sequence 197, App
106	29	69.0	917	7	US-11-205-935-20	Sequence 20, Appl	179	28	66.7	1483	7	US-11-188-298-10839	Sequence 10839, A
107	29	69.0	917	7	US-11-205-935-24	Sequence 24, Appl	180	28	66.7	1518	7	US-11-087-099-1886	Sequence 1886, Ap
108	29	69.0	917	7	US-11-205-935-26	Sequence 26, Appl	181	28	66.7	1827	7	US-11-057-058-62	Sequence 62, Appl
109	29	69.0	1306	6	US-10-995-561-905	Sequence 905, App	182	28	66.7	2051	6	US-10-330-773-307	Sequence 307, App
110	29	69.0	1356	6	US-10-995-561-906	Sequence 906, App	183	28	66.7	2304	6	US-10-330-773-310	Sequence 310, App
111	29	69.0	1356	6	US-10-995-561-906	Sequence 906, App	184	27	64.3	55	7	US-11-181-567A-8	Sequence 8, Appl
112	29	69.0	1410	6	US-10-878-556A-136	Sequence 136, App	185	27	64.3	85	7	US-11-096-568A-7502	Sequence 7502, Ap
113	29	69.0	1866	6	US-10-821-234-901	Sequence 136, App	186	27	64.3	92	7	US-11-072-512-2247	Sequence 2247, Ap
114	29	69.0	2830	7	US-11-186-731-2	Sequence 2, Appl	187	27	64.3	102	7	US-11-072-512-2358	Sequence 2358, Ap
115	29	69.0	4495	6	US-10-453-372-1002	Sequence 1002, Ap	188	27	64.3	126	6	US-10-793-626-2738	Sequence 2738, Ap
116	29	69.0	5636	7	US-11-065-695-20	Sequence 20, Appl	189	27	64.3	167	7	US-11-096-568A-3391	Sequence 3391, Ap
117	29	69.0	7968	7	US-11-186-731-5	Sequence 5, Appl	190	27	64.3	172	7	US-11-096-568A-24960	Sequence 24960, A
118	28	66.7	8	7	US-11-004-399-3150	Sequence 3150, Ap	191	27	64.3	183	7	US-11-096-568A-7218	Sequence 7218, Ap
119	28	66.7	55	6	US-10-467-657-2926	Sequence 2926, Ap	192	27	64.3	185	7	US-11-096-568A-24959	Sequence 24959, A
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121	28	66.7	163	7	US-11-188-298-7696	Sequence 7696, Ap	194	27	64.3	195	6	US-10-467-657-8594	Sequence 8594, Ap
122	28	66.7	178	7	US-11-188-298-4139	Sequence 4139, Ap	195	27	64.3	197	7	US-11-198-685-12	Sequence 12, Appl
123	28	66.7	188	7	US-11-188-298-4364	Sequence 4364, Ap	196	27	64.3	197	7	US-11-198-069-12	Sequence 28345, A
124	28	66.7	213	7	US-11-188-298-1886	Sequence 1886, Ap	197	27	64.3	210	7	US-11-096-568A-28345	Sequence 28344, A
125	28	66.7	214	7	US-11-122-396-29	Sequence 29, Appl	198	27	64.3	216	7	US-11-096-568A-28344	Sequence 28343, Ap
126	28	66.7	228	6	US-10-194-487-114	Sequence 114, App	199	27	64.3	248	7	US-11-096-568A-3390	Sequence 3390, Ap
127	28	66.7	228	6	US-10-195-883-114	Sequence 114, App	200	27	64.3	248	7	US-11-096-568A-28343	Sequence 28343, A
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141	28	66.7	342	7	US-11-096-568A-19662	Sequence 19662, A	214	27	64.3	326	7	US-11-096-568A-5723	Sequence 5723, Ap
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143	28	66.7	357	7	US-11-188-298-2278	Sequence 2278, Ap	216	27	64.3	335	7	US-11-096-568A-8475	Sequence 8475, Ap
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146	28	66.7	361	7	US-11-188-298-2272	Sequence 2272, Ap	219	27	64.3	342	7	US-11-096-568A-7217	Sequence 7217, Ap
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151	28	66.7	435	6	US-11-188-298-8860	Sequence 8860, Ap	224	27	64.3	348	7	US-11-188-298-15790	Sequence 15790, A
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154	28	66.7	474	7	US-11-096-568A-22472	Sequence 22472, A	227	27	64.3	368	7	US-11-096-568A-29973	Sequence 29973, A
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164	28	66.7	574	6	US-10-195-883-234	Sequence 234, App	237	27	64.3	405	7	US-11-096-568A-24244	Sequence 24244, A
165	28	66.7	580	6	US-10-195-883-234	Sequence 234, App	238	27	64.3	407	7	US-11-096-568A-13065	Sequence 13065, A
166	28	66.7	587	6	US-11-045-208-37	Sequence 37, Appl	239	27	64.3	412	7	US-11-096-568A-14655	Sequence 14655, A
167	28	66.7	587	6	US-10-644-807-334	Sequence 334, App	240	27	64.3	419	7	US-11-171-531-2	Sequence 2, Appl
168	28	66.7	632	7	US-11-188-298-978	Sequence 978, App	241	27	64.3	420	7	US-11-188-298-3292	Sequence 3292, Ap
169	28	66.7	702	7	US-11-188-298-2115	Sequence 2115, Ap	242	27	64.3				
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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 7: /SID55/ptodata/2/pubpaa/US11 NEW PUB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	85.7	521	7	US-11-079-463-8917
2	35	83.3	227	6	US-10-498-026-76
3	34	81.0	446	7	US-11-166-412-67
4	34	81.0	457	6	US-10-877-346-49
5	34	81.0	458	6	US-10-877-346-51
6	33	78.6	53	6	US-10-895-064-2440
7	33	78.6	53	7	US-11-129-741-2440
8	33	78.6	502	7	US-11-098-686-10506
9	33	78.6	855	7	US-11-087-099-12274
10	33	78.6	1166	7	US-11-188-298-11021
11	33	78.6	1566	7	US-11-188-298-9022
12	32	76.2	385	7	US-11-188-298-20860
13	32	76.2	389	7	US-11-188-298-21334
14	32	76.2	405	7	US-11-079-463-6011
15	32	76.2	508	7	US-11-087-099-5716
16	31	73.8	51	6	US-10-467-657-3360
17	31	73.8	265	6	US-10-392-234A-54
18	31	73.8	265	6	US-10-392-234A-58
19	31	73.8	475	6	US-10-877-346-48
20	31	73.8	477	6	US-10-877-346-47
21	31	73.8	480	6	US-10-877-346-15
22	31	73.8	486	6	US-10-877-346-50
23	31	73.8	490	7	US-11-072-512-3841
24	31	73.8	619	7	US-11-096-568A-20917
25	31	73.8	625	7	US-11-096-568A-20916

26	31	73.8	719	7	US-11-096-568A-20915	Sequence 20915, A
27	31	73.8	990	7	US-11-188-298-2875	Sequence 2875, Ap
28	31	73.8	3588	6	US-10-995-561-672	Sequence 672, App
29	31	73.8	4346	6	US-10-995-561-671	Sequence 671, App
30	31	73.8	4347	6	US-10-995-561-670	Sequence 670, App
31	31	73.8	4390	7	US-11-169-041-169	Sequence 169, App
32	31	73.8	4419	6	US-10-821-234-1155	Sequence 1155, Ap
33	30	71.4	287	7	US-11-096-568A-23012	Sequence 23012, A
34	30	71.4	351	7	US-11-096-568A-23011	Sequence 23011, A
35	30	71.4	357	7	US-11-096-568A-23010	Sequence 23010, A
36	30	71.4	400	7	US-11-188-298-19938	Sequence 19938, A
37	30	71.4	419	7	US-11-188-298-16217	Sequence 16217, A
38	29	69.0	36	7	US-11-004-399-2396	Sequence 2396, Ap
39	29	69.0	125	7	US-11-096-568A-19603	Sequence 19603, A
40	29	69.0	132	6	US-10-793-626-1438	Sequence 1438, Ap
41	29	69.0	157	7	US-11-079-463-5645	Sequence 5645, Ap
42	29	69.0	180	7	US-11-188-298-6069	Sequence 6069, Ap
43	29	69.0	203	7	US-11-096-568A-11529	Sequence 11529, A
44	29	69.0	211	7	US-11-124-368A-175	Sequence 175, App
45	29	69.0	211	7	US-11-124-368A-176	Sequence 176, App
46	29	69.0	231	7	US-11-188-298-14354	Sequence 14354, A
47	29	69.0	242	7	US-11-188-298-3157	Sequence 3157, Ap
48	29	69.0	242	7	US-11-188-298-20705	Sequence 20705, A
49	29	69.0	252	7	US-11-079-463-8309	Sequence 8309, Ap
50	29	69.0	265	7	US-11-096-568A-24007	Sequence 24007, A
51	29	69.0	288	7	US-11-188-298-12842	Sequence 12842, A
52	29	69.0	290	7	US-11-013-592-2	Sequence 2, Appl
53	29	69.0	292	7	US-11-188-298-12136	Sequence 12136, A
54	29	69.0	300	7	US-11-188-298-1074	Sequence 1074, Ap
55	29	69.0	301	7	US-11-096-568A-24006	Sequence 24006, A
56	29	69.0	307	7	US-11-096-568A-11528	Sequence 11528, A
57	29	69.0	309	7	US-11-087-099-4759	Sequence 4759, Ap
58	29	69.0	310	7	US-11-087-099-6235	Sequence 6235, Ap
59	29	69.0	310	7	US-11-087-099-12084	Sequence 12084, A
60	29	69.0	311	7	US-11-096-568A-7222	Sequence 7222, Ap
61	29	69.0	327	7	US-11-087-099-5493	Sequence 5493, Ap
62	29	69.0	330	7	US-11-074-176-174	Sequence 174, App
63	29	69.0	330	7	US-11-087-099-2823	Sequence 2823, Ap
64	29	69.0	332	7	US-11-087-099-3470	Sequence 3470, Ap
65	29	69.0	332	7	US-11-096-568A-11527	Sequence 11527, A
66	29	69.0	350	7	US-11-188-298-335	Sequence 335, App
67	29	69.0	363	7	US-11-188-298-6356	Sequence 6356, Ap
68	29	69.0	381	6	US-10-501-035-223	Sequence 223, App
69	29	69.0	389	7	US-11-188-298-572	Sequence 572, App
70	29	69.0	391	7	US-11-188-298-1874	Sequence 1874, Ap
71	29	69.0	391	7	US-11-087-099-11242	Sequence 11242, A
72	29	69.0	391	7	US-11-188-298-21372	Sequence 21372, A
73	29	69.0	393	7	US-11-188-298-11893	Sequence 11893, A
74	29	69.0	398	6	US-10-821-234-1583	Sequence 1583, Ap
75	29	69.0	398	7	US-11-188-298-745	Sequence 745, App
76	29	69.0	399	7	US-11-188-298-5102	Sequence 5102, Ap
77	29	69.0	400	7	US-11-188-298-8836	Sequence 8836, Ap
78	29	69.0	404	7	US-11-188-298-19850	Sequence 19850, A
79	29	69.0	405	7	US-11-087-099-11914	Sequence 11914, A
80	29	69.0	421	7	US-11-214-199-14	Sequence 14, Appl
81	29	69.0	429	7	US-11-096-568A-7221	Sequence 7221, Ap
82	29	69.0	435	7	US-11-079-463-7935	Sequence 7935, Ap
83	29	69.0	456	7	US-11-188-298-21690	Sequence 21690, A
84	29	69.0	457	6	US-10-467-657-6640	Sequence 6640, Ap
85	29	69.0	478	7	US-11-098-686-10724	Sequence 10724, A
86	29	69.0	481	7	US-11-096-568A-7220	Sequence 7220, Ap
87	29	69.0	502	7	US-11-096-568A-24189	Sequence 24189, A
88	29	69.0	519	7	US-11-096-568A-24188	Sequence 24188, A
89	29	69.0	542	7	US-11-013-592-40	Sequence 40, Appl
90	29	69.0	566	7	US-11-096-568A-24187	Sequence 24187, A
91	29	69.0	764	7	US-11-104-110-8	Sequence 8, Appl
92	29	69.0	764	7	US-11-104-111-28	Sequence 28, Appl
93	29	69.0	767	7	US-11-075-047A-4	Sequence 4, Appl
94	29	69.0	767	7	US-11-075-047A-4	Sequence 2, Appl
95	29	69.0	816	7	US-11-090-439-48	Sequence 48, Appl
96	29	69.0	915	7	US-11-144-987-16	Sequence 16, Appl
97	29	69.0	915	7	US-11-144-987-22	Sequence 22, Appl
98	29	69.0	915	7	US-11-144-987-22	Sequence 22, Appl

101	32	76.2	108	3	US-09-764-891-2829	Sequence 2829, Ap	174	31	73.8	291	4	US-10-425-115-248197	Sequence 248197,
102	32	76.2	108	4	US-10-091-438-190	Sequence 190, App	175	31	73.8	310	4	US-10-425-115-248197	Sequence 248197,
103	32	76.2	125	3	US-09-864-408A-2444	Sequence 2444, Ap	176	31	73.8	327	5	US-10-764-260-8	Sequence 8, Appli
104	32	76.2	155	4	US-10-437-963-163298	Sequence 163298,	177	31	73.8	327	5	US-10-764-260-9	Sequence 9, Appli
105	32	76.2	190	4	US-10-437-963-193374	Sequence 193374,	178	31	73.8	330	5	US-10-472-928-4104	Sequence 4104, Ap
106	32	76.2	212	4	US-10-768-093-7	Sequence 7, Appli	179	31	73.8	332	4	US-10-474-776-722	Sequence 722, App
107	32	76.2	217	4	US-10-424-599-284928	Sequence 284928,	180	31	73.8	335	4	US-10-017-161-694	Sequence 694, App
108	32	76.2	230	4	US-10-282-122A-68045	Sequence 68045, A	181	31	73.8	355	4	US-10-017-161-722	Sequence 722, App
109	32	76.2	296	4	US-10-425-115-266787	Sequence 266787,	182	31	73.8	355	4	US-10-017-161-722	Sequence 722, App
110	32	76.2	326	4	US-10-369-493-9804	Sequence 9804, Ap	183	31	73.8	357	4	US-10-292-798-632	Sequence 632, App
111	32	76.2	383	3	US-09-939-853A-22	Sequence 22, Appli	184	31	73.8	357	4	US-10-292-798-632	Sequence 632, App
112	32	76.2	425	4	US-10-437-963-176705	Sequence 176705,	185	31	73.8	388	4	US-10-425-115-286991	Sequence 286991,
113	32	76.2	432	4	US-10-289-762-321	Sequence 321, App	186	31	73.8	388	4	US-10-425-115-286991	Sequence 286991,
114	32	76.2	438	4	US-10-282-122A-52465	Sequence 52465, A	187	31	73.8	394	4	US-09-817-513A-4	Sequence 4, Appli
115	32	76.2	464	5	US-10-732-923-6308	Sequence 6308, Ap	188	31	73.8	416	4	US-10-425-114-64456	Sequence 64456, A
116	32	76.2	479	4	US-10-282-122A-51794	Sequence 51794, A	189	31	73.8	455	4	US-10-282-122A-60545	Sequence 60545, A
117	32	76.2	505	4	US-10-437-963-115721	Sequence 115721,	190	31	73.8	463	4	US-10-282-122A-46851	Sequence 46851, A
118	32	76.2	511	3	US-09-893-519A-23	Sequence 23, Appli	191	31	73.8	475	3	US-09-964-956-48	Sequence 5, Appli
119	32	76.2	511	4	US-10-369-493-1888	Sequence 1888, Ap	192	31	73.8	475	3	US-09-964-956-48	Sequence 5, Appli
120	32	76.2	591	4	US-10-424-599-285635	Sequence 285635,	193	31	73.8	477	3	US-10-299-642-24	Sequence 24, Appli
121	32	76.2	614	4	US-10-369-493-10317	Sequence 10317, A	194	31	73.8	477	3	US-09-826-505-493	Sequence 493, App
122	32	76.2	661	4	US-10-160-865-14	Sequence-14, Appli	195	31	73.8	477	3	US-09-964-956-47	Sequence 47, Appli
123	32	76.2	761	5	US-10-732-923-15033	Sequence 15033, A	196	31	73.8	477	4	US-10-277-078-2	Sequence 2, Appli
124	32	76.2	905	4	US-10-425-115-313616	Sequence 313616,	197	31	73.8	477	4	US-10-277-078-2	Sequence 2, Appli
125	32	76.2	928	4	US-10-425-114-60524	Sequence 60524, A	198	31	73.8	477	4	US-10-277-078-2	Sequence 2, Appli
126	32	76.2	1091	4	US-10-425-115-284004	Sequence 284004, A	199	31	73.8	477	4	US-10-277-078-2	Sequence 2, Appli
127	32	76.2	1193	4	US-10-437-963-197504	Sequence 197504,	200	31	73.8	477	5	US-10-299-642-8	Sequence 8, Appli
128	32	76.2	1201	4	US-10-437-963-129457	Sequence 129457,	201	31	73.8	486	3	US-10-352-684A-4	Sequence 4, Appli
129	32	76.2	1297	4	US-10-425-115-313614	Sequence 313614,	202	31	73.8	486	3	US-10-352-684A-4	Sequence 4, Appli
130	32	76.2	1449	4	US-10-389-566-2124	Sequence 2124, Ap	203	31	73.8	488	5	US-10-450-763-50437	Sequence 7, Appli
131	32	76.2	1902	6	US-11-097-143-22953	Sequence 22953, A	204	31	73.8	490	4	US-10-168-655-7	Sequence 7, Appli
132	32	76.2	2046	4	US-10-425-115-235423	Sequence 235423,	205	31	73.8	490	4	US-10-168-655-7	Sequence 7, Appli
133	32	76.2	3186	4	US-10-210-130-34	Sequence 34, Appli	206	31	73.8	490	4	US-10-168-655-7	Sequence 7, Appli
134	32	76.2	3208	4	US-10-210-130-36	Sequence 36, Appli	207	31	73.8	540	4	US-10-112-944-876	Sequence 876, App
135	32	76.2	3267	5	US-10-491-467-28	Sequence 28, Appli	208	31	73.8	540	4	US-10-112-944-876	Sequence 876, App
136	32	76.2	3268	4	US-10-379-381-2	Sequence 2, Appli	209	31	73.8	577	5	US-10-450-763-53621	Sequence 53621, A
137	32	76.2	36946	5	US-10-074-475-229	Sequence 229, App	210	31	73.8	585	4	US-10-450-763-53621	Sequence 53621, A
138	32	76.2	41	4	US-10-425-115-208283	Sequence 208283,	211	31	73.8	587	4	US-10-450-763-53621	Sequence 53621, A
139	31	73.8	43	4	US-10-425-115-208283	Sequence 208283,	212	31	73.8	622	4	US-10-450-763-53621	Sequence 53621, A
140	31	73.8	45	4	US-10-424-599-162493	Sequence 162493,	213	31	73.8	624	4	US-10-450-763-53621	Sequence 53621, A
141	31	73.8	55	4	US-10-437-963-157644	Sequence 157644,	214	31	73.8	713	3	US-10-437-963-170425	Sequence 170425,
142	31	73.8	64	4	US-10-437-963-151058	Sequence 151058,	215	31	73.8	713	3	US-10-437-963-170425	Sequence 170425,
143	31	73.8	68	3	US-09-864-761-46592	Sequence 46592, A	216	31	73.8	775	3	US-09-882-227-112	Sequence 112, App
144	31	73.8	68	4	US-10-437-963-174975	Sequence 174975,	217	31	73.8	775	3	US-09-882-227-112	Sequence 112, App
145	31	73.8	68	4	US-10-425-115-226663	Sequence 226663,	218	31	73.8	776	4	US-10-335-977-7035	Sequence 7035, Ap
146	31	73.8	68	4	US-10-425-115-226663	Sequence 226663,	219	31	73.8	776	4	US-10-335-977-7035	Sequence 7035, Ap
147	31	73.8	92	4	US-10-424-599-225637	Sequence 225637,	220	31	73.8	793	6	US-11-097-143-37410	Sequence 37410, A
148	31	73.8	144	4	US-10-106-698-5264	Sequence 5264, Ap	221	31	73.8	803	4	US-10-282-122A-58178	Sequence 58178, A
149	31	73.8	150	4	US-10-425-114-43790	Sequence 43790, A	222	31	73.8	803	4	US-10-282-122A-58178	Sequence 58178, A
150	31	73.8	164	4	US-10-437-963-108661	Sequence 108661,	223	31	73.8	829	4	US-10-369-493-14754	Sequence 14754, A
151	31	73.8	165	4	US-10-767-701-36935	Sequence 36935, A	224	31	73.8	830	4	US-10-369-493-14754	Sequence 14754, A
152	31	73.8	174	4	US-10-017-161-700	Sequence 700, App	225	31	73.8	834	4	US-10-369-493-15233	Sequence 15233, A
153	31	73.8	174	4	US-10-292-798-612	Sequence 612, App	226	31	73.8	850	4	US-10-369-493-15233	Sequence 15233, A
154	31	73.8	178	4	US-10-292-798-606	Sequence 606, App	227	31	73.8	850	4	US-10-369-493-15233	Sequence 15233, A
155	31	73.8	185	4	US-10-437-963-203299	Sequence 203299,	228	31	73.8	1062	4	US-10-450-763-45268	Sequence 45268, A
156	31	73.8	196	3	US-09-764-870-396	Sequence 396, App	229	31	73.8	1064	5	US-10-450-763-45268	Sequence 45268, A
157	31	73.8	196	4	US-10-125-540-396	Sequence 540, App	230	31	73.8	1076	5	US-10-450-763-45268	Sequence 45268, A
158	31	73.8	197	4	US-10-425-114-37134	Sequence 37134, A	231	31	73.8	1076	5	US-10-450-763-45268	Sequence 45268, A
159	31	73.8	202	3	US-09-764-875-631	Sequence 631, App	232	31	73.8	1076	5	US-10-450-763-45268	Sequence 45268, A
160	31	73.8	204	3	US-09-847-208-166	Sequence 166, App	233	31	73.8	1076	5	US-10-450-763-45268	Sequence 45268, A
161	31	73.8	204	3	US-10-091-135-66	Sequence 66, Appli	234	31	73.8	1138	4	US-10-450-763-45268	Sequence 45268, A
162	31	73.8	213	4	US-10-335-977-7030	Sequence 7030, Ap	235	31	73.8	1138	4	US-10-450-763-45268	Sequence 45268, A
163	31	73.8	219	4	US-10-767-701-36370	Sequence 36370, A	236	31	73.8	1240	5	US-10-450-763-45268	Sequence 45268, A
164	31	73.8	227	4	US-10-424-599-285634	Sequence 285634,	237	31	73.8	1240	5	US-10-450-763-45268	Sequence 45268, A
165	31	73.8	250	4	US-10-156-761-13009	Sequence 13009, A	238	31	73.8	1240	5	US-10-450-763-45268	Sequence 45268, A
166	31	73.8	257	4	US-10-425-114-49413	Sequence 49413, A	239	31	73.8	1240	5	US-10-450-763-45268	Sequence 45268, A
167	31	73.8	257	6	US-11-097-143-5151	Sequence 5151, Ap	240	31	73.8	1395	5	US-10-732-923-2913	Sequence 2913, Ap
168	31	73.8	265	3	US-09-870-759-108	Sequence 108, App	241	31	73.8	1395	5	US-10-732-923-2913	Sequence 2913, Ap
169	31	73.8	265	3	US-09-751-708A-108	Sequence 108, App	242	31	73.8	1466	6	US-10-450-763-36985	Sequence 36985, A
170	31	73.8	285	4	US-10-428-817A-104	Sequence 104, App	243	31	73.8	1466	6	US-10-450-763-36985	Sequence 36985, A
171	31	73.8	285	5	US-10-937-758A-85	Sequence 85, Appli	244	31	73.8	2055	6	US-11-097-143-37410	Sequence 37410, A
172	31	73.8	284	4	US-10-424-599-226130	Sequence 226130,	245	31	73.8	2055	6	US-11-097-143-37410	Sequence 37410, A
173	31	73.8	291	4	US-10-437-963-189875	Sequence 189875,	246	31	73.8	2055	6	US-11-097-143-37410	Sequence 37410, A

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:28:34 ; Search time 41.125 Seconds
(without alignments)
71.120 Million cell updates/sec

Title: US-10-091-135-12
Perfect score: 42
Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	42	100.0	7	4	US-10-091-135-12
2	38	90.5	55	4	US-10-437-963-191029
3	37	88.1	192	4	US-10-001-245-122
4	36	85.7	170	4	US-10-425-114-50955
5	36	85.7	222	4	US-10-425-114-55971
6	36	85.7	284	5	US-10-732-923-6302
7	36	85.7	513	4	US-10-282-122A-48629
8	36	85.7	739	4	US-10-424-599-262939
9	35	83.3	49	4	US-10-091-135-8
10	35	83.3	198	4	US-10-001-245-121
11	35	83.3	201	4	US-10-001-245-119
12	35	83.3	202	4	US-10-001-245-117
13	35	83.3	203	4	US-10-001-245-118
14	35	83.3	204	3	US-09-847-208-162
15	35	83.3	204	3	US-09-847-208-163
16	35	83.3	204	4	US-10-091-135-16
17	35	83.3	204	4	US-10-091-135-64
18	35	83.3	204	4	US-10-091-135-65
19	35	83.3	204	4	US-10-091-135-67
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21	35	83.3	204	4	US-10-719-553-39
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	34	81.0	446	Sequence 4, Appl
15	34	81.0	446	Sequence 4, Appl
16	34	81.0	446	Sequence 487, App
17	34	81.0	446	Sequence 4, Appl
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52	31	73.8	477	2	US-09-964-956-47	Sequence 47, Appl
53	31	73.8	477	2	US-10-277-078-2	Sequence 2, Appl
54	31	73.8	477	2	US-10-277-078-3	Sequence 3, Appl
55	31	73.8	486	2	US-09-964-956-15	Sequence 15, Appl
56	31	73.8	486	2	US-09-964-956-50	Sequence 50, Appl
57	31	73.8	490	2	US-10-104-047-3841	Sequence 3841, Ap
58	31	73.8	490	2	US-09-328-352-4432	Sequence 4432, Ap
59	31	73.8	4391	2	US-10-006-011A-2	Sequence 2, Appl
60	30	71.4	11	1	US-07-920-519-13	Sequence 13, Appl
61	30	71.4	11	1	US-08-086-410-10	Sequence 10, Appl
62	30	71.4	11	1	US-08-314-596-13	Sequence 13, Appl
63	30	71.4	17	1	US-07-920-519-17	Sequence 17, Appl
64	30	71.4	17	1	US-08-086-410-14	Sequence 14, Appl
65	30	71.4	17	1	US-08-314-586-17	Sequence 17, Appl
66	30	71.4	20	1	US-08-614-935-75	Sequence 75, Appl
67	30	71.4	20	2	US-09-130-287-75	Sequence 75, Appl
68	30	71.4	76	2	US-09-489-039A-13231	Sequence 13231, A
69	30	71.4	123	2	US-09-205-258-780	Sequence 780, App
70	30	71.4	123	2	US-10-004-860-780	Sequence 780, App
71	30	71.4	141	2	US-09-328-352-5789	Sequence 5789, Ap
72	30	71.4	143	2	US-09-270-767-37046	Sequence 37046, A
73	30	71.4	143	2	US-09-270-767-52263	Sequence 52263, A
74	30	71.4	168	2	US-09-270-767-34036	Sequence 34036, A
75	30	71.4	168	2	US-09-270-767-49253	Sequence 49253, A
76	30	71.4	204	1	US-08-614-935-1	Sequence 1, Appl
77	30	71.4	204	2	US-09-130-287-1	Sequence 1, Appl
78	30	71.4	241	2	US-09-107-532A-5876	Sequence 5876, Ap
79	30	71.4	253	2	US-09-270-767-35268	Sequence 35268, A
80	30	71.4	253	2	US-09-270-767-50485	Sequence 50485, A
81	30	71.4	301	1	US-07-920-519-1	Sequence 1, Appl
82	30	71.4	301	1	US-08-314-586-1	Sequence 1, Appl
83	30	71.4	302	1	US-07-920-519-2	Sequence 2, Appl
84	30	71.4	302	1	US-08-086-410-37	Sequence 37, Appl
85	30	71.4	302	1	US-08-314-586-2	Sequence 2, Appl
86	30	71.4	302	1	US-08-314-586-40	Sequence 40, Appl
87	30	71.4	302	1	US-09-347-878-58	Sequence 58, Appl
88	30	71.4	311	2	US-09-252-991A-18334	Sequence 18334, A
89	30	71.4	409	2	US-09-270-767-38540	Sequence 38540, A
90	30	71.4	456	2	US-09-240-639-2	Sequence 2, Appl
91	30	71.4	456	2	US-09-908-510A-2	Sequence 2, Appl
92	30	71.4	456	2	US-09-905-744B-2	Sequence 2, Appl
93	30	71.4	456	2	US-10-107-660-2	Sequence 2, Appl
94	30	71.4	456	2	US-10-107-576-2	Sequence 2, Appl
95	30	71.4	456	2	US-09-905-732B-2	Sequence 2, Appl
96	30	71.4	456	2	US-09-905-743B-2	Sequence 2, Appl
97	30	71.4	456	2	US-09-905-589-2	Sequence 2, Appl
98	30	71.4	456	2	US-09-108-171A-2	Sequence 2, Appl
99	30	71.4	471	2	US-09-608-285A-60	Sequence 60, Appl
100	30	71.4	471	2		

105	33	78.6	343	2	Q9VT93_DROME	Q9vt93_drosophila	178	32	76.2	297	2	Q81YK0_BACAN	O81yk0_bacillus an
106	33	78.6	348	2	O99595_ARTJA	O99595 artibeus ja	179	32	76.2	304	2	Q7TIF2_CHICK	Q7tif2 gallus gall
107	33	78.6	350	2	O5GULO_XANAC	O5gulo_xanthomonas	180	32	76.2	307	1	YSCQ_YERPS	P42713 yersinia pe
108	33	78.6	350	2	O8PFR5_XANAC	O8pfr5_xanthomonas	181	32	76.2	309	1	YSCQ_YERPS	P40296 yersinia pe
109	33	78.6	380	2	O42317_CYPCA	O42317 cyprinus ca	182	32	76.2	317	2	Q4SDY7_TETNG	O4sdy7 tetraodon n
110	33	78.6	398	2	O8RFR3_FUSNN	O8rfr3_fusobacteri	183	32	76.2	325	2	Q8XJ57_CLOPE	O8xj57 clostridium
111	33	78.6	410	1	ODO2_BUCBP	O89aj6_buchnera ap	184	32	76.2	332	2	Q9GUE4_CAEEL	O9gue4 caenorhabdi
112	33	78.6	411	2	O8T476_DROME	O8t476_drosophila	185	32	76.2	342	2	Q7PKI7_ANO	O7pki7 anopheles g
113	33	78.6	424	2	Q4NDL4_9MICC	Q4ndl4_arthrobacte	186	32	76.2	344	2	Q4J0B6_AZOVI	Q4j0b6 azotobacter
114	33	78.6	430	2	Q60UD3_CAEER	Q60ud3_caenorhabdi	187	32	76.2	345	2	Q4UEL4_THEAN	Q4uel4 theileria a
115	33	78.6	433	2	Q6WAB4_PARUW	Q6wab4_parachlamyd	188	32	76.2	359	1	REBG_SALTY	P82397 salmonella
116	33	78.6	444	2	Q7LZ73_CHICK	Q7l7z3_gallus gall	189	32	76.2	359	2	Q8Z5I5_SALTI	P26397 salmonella
117	33	78.6	444	2	Q54VQ5_DICDI	Q54vq5_dictyosteli	190	32	76.2	359	2	Q5PE01_SALPA	Q5pe01 salmoneila
118	33	78.6	463	2	O54IJ3_DICDI	O54ij3_dictyosteli	191	32	76.2	378	2	Q5OH17_ACTPL	Q5oh17 actinobacil
119	33	78.6	466	1	DCEA_ECO57	P58228 escherichia	192	32	76.2	379	2	Q4IQ70_GIBZE	Q4iq70 gibzella
120	33	78.6	466	1	DCEA_ECOL6	P69909 escherichia	193	32	76.2	380	2	Q5OH23_ACTPL	Q5oh23 actinobacil
121	33	78.6	466	1	DCEA_ECOLI	P69908 escherichia	194	32	76.2	381	2	Q6UYC5_ACTPL	Q6uyc5 actinobacil
122	33	78.6	466	1	DCEA_SHIFL	P69908 escherichia	195	32	76.2	382	2	Q74339_SCHPO	Q74339 schizosacch
123	33	78.6	466	1	DCEB_ECOL6	P69910 escherichia	196	32	76.2	383	2	Q6V013_ACTPL	Q6v013 actinobacil
124	33	78.6	466	1	DCEB_ECOLI	P69912 shigella fl	197	32	76.2	385	2	Q4IIE1_GIBZE	Q4iie1 gibzella
125	33	78.6	466	1	DCEB_SHIFL	Q6arb0_desulfotale	198	32	76.2	389	2	P70778_9NOSP	P70778 anabaena ep
126	33	78.6	474	2	Q6ARB0_DESPS	Q6fsg1_candida gla	199	32	76.2	389	2	Q7A2B1_9NOSP	Q7a2b1 anabaena ep
127	33	78.6	513	2	Q6FSG1_CANGA	Q7pxg5_anopheles g	200	32	76.2	389	2	Q8YRP4_9NOSP	Q8yrp4 anabaena ep
128	33	78.6	513	2	Q7PXQ5_9CAUD	Q8w6y9_cyanophag	201	32	76.2	389	2	Q8YRP4_9NOSP	Q8yrp4 anabaena ep
129	33	78.6	513	2	Q8W6Y9_9CAUD	Q51lq4_magnaporthe	202	32	76.2	391	2	Q9R6X5_9NOSP	Q9r6x5 myxine glut
130	33	78.6	555	2	O51LQ4_MAGGR	Q6ckf5_kluyveromyc	203	32	76.2	392	2	Q9YH45_MXGL	Q9y4h5 mantheimia
131	33	78.6	562	2	Q7NEN1_MYCGA	O6ckf5_kluyveromyc	204	32	76.2	397	2	Q6J5U9_9NOSP	Q6j5u9 synchocyst
132	33	78.6	577	2	Q6CKF5_KLUJA	Q7vae2_prochloroco	205	32	76.2	402	2	Q94JQ9_9NOSP	Q94jq9 mantheimia
133	33	78.6	593	2	Q7VAE2_PROMA	Q6f4v1_candida gla	206	32	76.2	409	2	P73556_SYNY3	P73556 synchocyst
134	33	78.6	667	2	Q6FV41_CANGA	Q6l2u8_caenorhabdi	207	32	76.2	411	2	Q9KT34_VIBCH	Q9kt34 vibrio chol
135	33	78.6	673	2	Q6FV41_CANGA	Q6l2u8_caenorhabdi	208	32	76.2	420	1	ODO2_BUCAL	O823e3 chlamydomph
136	33	78.6	689	2	Q6L2U8_CAEER	Q69vk3_oryza sativ	209	32	76.2	428	2	Q82PE3_CHLCV	Q82pe3 chlamydomph
137	33	78.6	689	2	Q6L2U8_CAEER	Q936k0_rhizobium l	210	32	76.2	428	2	Q9PKE7_CHLMU	Q9pke7 chlamydomph
138	33	78.6	723	2	Q69VK3_ORYSA	Q6bte9_debaryomyce	211	32	76.2	429	2	Q5L616_CHLAB	Q5l616 chlamydomph
139	33	78.6	855	2	Q936K0_RHILE	O9p4e0_ustilago ma	212	32	76.2	431	2	Q928N2_CHLNP	Q928n2 chlamydomph
140	33	78.6	1041	2	O6BTC9_DEBHA	O9p4e0_ustilago ma	213	32	76.2	431	2	Q7JMW5_CAEEL	Q7jmw5 caenorhabdi
141	33	78.6	1166	2	O9PAE0_USTWA	O57261_trypanosoma	214	32	76.2	448	2	Q5NEB8_FRAAT	Q5neb8 franciella
142	33	78.6	1233	2	O57261_9TRYP	Q8j230_ustilago ma	215	32	76.2	451	2	Q9LITE6_9NOSP	Q9lite6 arabisopsis
143	33	78.6	1566	2	Q8J230_USTWA	Q4p8k5_ustilago ma	216	32	76.2	453	2	Q5UW77_HALMA	Q5uw77 halorcula
144	33	78.6	1568	2	Q4P6K5_USTWA	O5scv7_huperzia lu	217	32	76.2	454	2	Q73PZ4_WOLPM	Q73pz4 wolbachia p
145	33	78.6	1665	2	O5SCV7_HUPLU	O7jms1_caenorhabdi	218	32	76.2	460	2	O5LH38_BACFR	O5lh38 bacteroides
146	33	78.6	1665	2	Q7JM51_CAEEL	O8mm09_caenorhabdi	219	32	76.2	460	2	O64XZ5_BACFR	O64xz5 bacteroides
147	33	78.6	1868	2	O8MM09_CAEEL	O60z22_caenorhabdi	220	32	76.2	463	2	Q8A169_BACTN	O8a169 bacteroides
148	33	78.6	1895	2	O60Z22_CAEER	O9tvi2_caenorhabdi	221	32	76.2	464	2	Q8NFB8_CORDI	Q8nfb8 corynebacte
149	33	78.6	1896	2	Q9TVI2_CAEEL	Q5aw12_aspergillus	222	32	76.2	464	2	Q5E5Y7_VIBF1	Q5e5y7 vibrio fisc
150	33	78.6	3043	2	Q5AW12_EMENI	Q49852_mycobacteri	223	32	76.2	464	2	Q8GF15_EDWTA	Q8gf15 edwardsiell
151	33	76.2	49	2	Q49852_MYCLE	O5w2n4_sulfolobus	224	32	76.2	479	2	Q97IG7_CLOAB	Q97ig7 clostridium
152	33	76.2	83	2	Q5W2N4_SULIS	O6261_mycobacteri	225	32	76.2	487	2	Q9SKY1_9NOSP	Q9sky1 arabisopsis
153	33	76.2	100	2	Q7TWH8_MYCBO	O9ccv7_mycobacteri	226	32	76.2	505	2	Q6ZD63_ORYSA	Q6z463 oryza sativ
154	33	76.2	100	2	O6Z611_MYCTU	Q9ccv7_mycobacteri	227	32	76.2	511	1	RRB1_YEAST	O04225 saccharomyc
155	33	76.2	104	2	Q9CCV7_MYCLE	Q9ccv7_rickettsia	228	32	76.2	512	2	O13985_SCHPO	O13985 schizosacch
156	33	76.2	108	1	Y826_RICPR	Q4g4c4_edwardsiell	229	32	76.2	512	2	O6FN01_CANGA	O6fn01 candida gla
157	33	76.2	122	2	Q4G4C4_EDWTA	Q720b0_listeria mo	230	32	76.2	521	2	Q759N3_9NOSP	Q759n3 ashbya goss
158	33	76.2	124	2	Q720B0_LISMF	O8y7g8_listeria mo	231	32	76.2	523	2	O6CJN4_KLUJA	O6cjin4 kluyveromyc
159	33	76.2	124	2	O8Y7G8_LISMO	O6g432_bartonella	232	32	76.2	530	2	Q9FUF3_SOYBN	Q9fuf3 glycine max
160	33	76.2	124	2	O6G492_BARHE	Q6k3h2_oryza sativ	233	32	76.2	676	2	Q418V5_GIBZE	Q418v5 gibzella
161	33	76.2	152	2	Q6K3H2_ORYSA	Q747u1_geobactera s	234	32	76.2	728	2	Q4FQY5_9NOSP	Q4fy5 psychrobact
162	33	76.2	155	2	Q747U1_GEOSL	Q73qf3_treponema d	235	32	76.2	738	2	P79190_BO5PR	P79190 bos primige
163	33	76.2	161	2	Q73QF3_TREDE	Q44205_agrobacteri	236	32	76.2	739	1	PECA1_BOVIN	P51866 bos taurus
164	33	76.2	173	2	Q44205_AGRRH	Q4hk13_campylobact	237	32	76.2	761	2	Q8S3S4_ORYSA	Q8s3s4 oryza sativ
165	33	76.2	205	2	O4HK13_CAMLA	O7x4h6_pseudomonas	238	32	76.2	761	2	Q8MB09_PARUW	Q8mb09 parachlamyd
166	33	76.2	230	2	Q7X4H6_PSEPU	P53518 escherichia	239	32	76.2	794	2	Q70G21_LACHE	Q70g21 lactobacill
167	33	76.2	232	1	CSSCI_ECOLI	P53519 escherichia	240	32	76.2	835	2	Q41865_MAIZE	Q41865 zea mays (m
168	33	76.2	232	1	CSSCI_ECOLI	P53519 escherichia	241	32	76.2	897	2	Q64828_9NOSP	Q64828 arabisopsis
169	33	76.2	232	2	Q88NL8_PSEPK	Q9hjn9_thermoplasm	242	32	76.2	907	2	O4Q348_LETHA	O4q348 leishmania
170	33	76.2	241	2	Q9HJ99_THEAC	P70915_bacillus in	243	32	76.2	932	2	Q6Q348_LETHA	Q6q348 leishmania
171	33	76.2	292	2	P70915_BACIN	O5zk93_gallus gall	244	32	76.2	986	2	Q5F3M0_CHICK	Q5f3m0 gallus gall
172	33	76.2	292	2	O5ZK93_CHICK	Q4my36_bacillus ce	245	32	76.2	1193	2	Q4JF22_ORYSA	Q4jf22 oryza sativ
173	33	76.2	292	2	Q4MY36_BACCE	Q637y2_bacillus ce	246	32	76.2	1197	2	Q9CAM1_9NOSP	Q9cam1 arabisopsis
174	33	76.2	297	2	O637Y2_BACCC	Q6hfu9_bacillus th	247	32	76.2	1198	2	Q6VY15_ORYSA	Q6vy15 oryza sativ
175	33	76.2	297	2	O6HFU9_BACHK	Q734b2_bacillus ce	248	32	76.2	1211	2	Q84XG3_MAIZE	Q84xg3 zea mays (m
176	33	76.2	297	2	Q734B2_BACCC	Q81at0_bacillus ce	249	32	76.2	1275	2	Q88Z88_LACPL	Q88z88 lactobacill
177	33	76.2	297	2	Q81AT0_BACCC		250	32	76.2	1296	2	Q7QJ29_9NOSP	Q7qj29 anopheles g

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 73.7917 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-12

Perfect score: 42

Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	92.9	61	2	Q42209 PLABE
2	39	92.9	363	1	DRD1_CARAU
3	38	90.5	240	2	Q97K74 CLOAB
4	37	88.1	162	2	Q7SD13_NEUCR
5	37	88.1	238	2	Q9UZA0_PYRAB
6	37	88.1	492	2	Q7RA59_PLAYO
7	36	85.7	161	2	Q5KU32_CLOCL
8	36	85.7	314	2	Q853P8_9CAUD
9	36	85.7	351	2	Q4UYZ6_XANCP
10	36	85.7	351	2	Q8F534_XANCP
11	36	85.7	428	2	Q19839_CABEL
12	36	85.7	513	2	Q5L1A2_BACFN
13	36	85.7	513	2	Q64ZB5_BACFR
14	36	85.7	513	2	Q8A1P8_BACTN
15	36	85.7	739	2	Q9M5J3_PHAAU
16	36	85.7	745	2	Q9ZRVR_CICAR
17	36	85.7	960	2	Q4S4N9_TETNG
18	35	83.3	204	1	VA5_VESFL
19	35	83.3	204	1	VA5_VESGE
20	35	83.3	227	1	VA5_VESVU
21	35	83.3	235	2	Q58D54_BOVIN
22	35	83.3	240	2	Q8C2X3_MOUSE
23	35	83.3	298	2	Q5UP69_MIMIV
24	35	83.3	393	1	CYH4_MOUSE
25	35	83.3	396	2	Q8IYW9_HUMAN
26	35	83.3	408	2	Q571J1_MOUSE
27	35	83.3	473	1	ABGA_CLOLO
28	35	83.3	487	2	Q4NRP0_9DELT
29	35	83.3	639	2	Q4P692_USTMA
30	35	83.3	735	2	Q6ZPT9_MOUSE
31	35	83.3	769	2	Q6LJF4_PHOPR

32	35	83.3	804	2	Q9CJW1_PASMU
33	35	83.3	822	2	Q7TQK8_MOUSE
34	35	83.3	889	2	Q9F2NS_HUMAN
35	35	83.3	961	2	Q8YQV0_ANASP
36	35	83.3	1005	2	Q5SFM8_MOUSE
37	35	83.3	1039	2	Q86NJ2_CAEEL
38	35	83.3	1184	2	Q86NJ3_CAEEL
39	35	83.3	1419	2	Q86NJ4_CAEEL
40	35	83.3	1658	2	Q9BIC1_CABEL
41	35	83.3	1666	2	Q9XY66_CABEL
42	34	81.0	61	2	Q9QVU0_9MURI
43	34	81.0	168	1	DRD1_BOVIN
44	34	81.0	178	2	Q4WN56_ASPFU
45	34	81.0	180	1	DRD1_RABIT
46	34	81.0	218	2	Q56HX9_9BACT
47	34	81.0	218	2	Q8GEP5_9BACT
48	34	81.0	218	2	Q9YHA9_MYXGL
49	34	81.0	240	2	Q9YHB0_PETMA
50	34	81.0	244	2	Q8XL70_CLOPE
51	34	81.0	247	2	Q97MD5_CLOAB
52	34	81.0	267	2	Q896N2_CLOTE
53	34	81.0	267	2	Q88U16_LACPL
54	34	81.0	309	2	Q4ST28_TETNG
55	34	81.0	320	2	Q8U676_AGRRT5
56	34	81.0	414	2	Q4SBH5_TETNG
57	34	81.0	429	2	Q84249_CHLTR
58	34	81.0	437	2	Q42316_CYPCA
59	34	81.0	445	2	Q98842_ANGAN
60	34	81.0	445	2	Q98841_ANGAN
61	34	81.0	446	1	DRD1_DIDMA
62	34	81.0	446	1	DRD1_HUMAN
63	34	81.0	446	1	DRD1_MACMU
64	34	81.0	446	1	DRD1_MOUSE
65	34	81.0	446	1	DRD1_PIG
66	34	81.0	446	1	DRD1_RAT
67	34	81.0	446	2	Q6FH34_HUMAN
68	34	81.0	446	2	Q4QRJ0_HUMAN
69	34	81.0	446	2	Q8WND7_BOVIN
70	34	81.0	446	2	Q42315_CYPCA
71	34	81.0	448	2	Q98844_ANGAN
72	34	81.0	450	2	Q7LZ75_CHICK
73	34	81.0	451	1	DRD1_XENLA
74	34	81.0	457	1	DRD5_XENLA
75	34	81.0	458	2	Q98843_ANGAN
76	34	81.0	458	2	Q4RIQ8_TETNG
77	34	81.0	459	1	DRD1L_FUGRU
78	34	81.0	465	1	DRD1C_XENLA
79	34	81.0	489	1	TAC2N_MOUSE
80	34	81.0	489	2	Q5M7U8_RAT
81	34	81.0	758	2	Q9D277_MOUSE
82	34	81.0	798	2	Q9U4E1_OXYNO
83	34	81.0	802	2	Q7VM53_HAEDU
84	34	81.0	865	2	Q8L614_ARATH
85	34	81.0	956	2	Q8R004_MOUSE
86	34	81.0	956	2	Q8WVF1_MOUSE
87	34	81.0	984	2	Q6NUW0_BRARE
88	34	81.0	987	2	Q99K74_MOUSE
89	34	81.0	987	2	Q4V8B3_RAT
90	34	81.0	989	1	T5100_HUMAN
91	34	81.0	1194	2	Q5FKY7_ARATH
92	34	81.0	1314	2	Q54S68_DICDI
93	33	78.6	72	2	Q5WRX2_LEGPL
94	33	78.6	92	2	Q87BQ8_XYLFT
95	33	78.6	98	2	Q73S32_MYCPA
96	33	78.6	174	2	Q7R1W8_GIALA
97	33	78.6	183	2	Q87ND8_VIBPA
98	33	78.6	193	1	YK02_YEAST
99	33	78.6	205	2	Q6MPA7_BDEBA
100	33	78.6	228	2	Q6OT06_CABBR
101	33	78.6	258	2	Q6K2U8_ORYZA
102	33	78.6	295	2	Q5LQ00_SILPO
103	33	78.6	309	2	Q5FJN9_LACAP
104	33	78.6	328	2	Q6UCZ6_9PROT

Q9CJm1	pasteurella
Q7Tqk8	mus musculus
Q92n5	homo sapien
Q8YqV0	anabaena sp
Q5Sfm8	mus musculus
Q86nj2	caenorhabdi
Q86nj3	caenorhabdi
Q86nj4	caenorhabdi
Q86ic1	caenorhabdi
Q9xy66	caenorhabdi
Q9QVU0	rattus sp.
Q95136	bos taurus
Q4wn56	aspergillus
O02664	oryctolagus
Q56hx9	uncultured
Q8Gep5	myxine glut
Q9Yha9	petromyzon
Q9Yhb0	petromyzon
Q8xl70	clostridium
Q97md5	clostridium
Q896n2	clostridium
Q88u16	lactobacill
Q4st28	tetradodon n
Q8u676	agrobacteri
Q4sbh5	tetradodon n
Q84249	chlamydia t
Q42316	cyprinus ca
Q98842	anguilla an
Q98841	anguilla an
P42288	delphis m
P21728	homo sapien
O77680	macaca mula
P61616	mus musculus
P50130	sus scrofa
P18901	rattus norv
Q6fh34	homo sapien
Q4qrj0	homo sapien
Q8wnd7	bos taurus
O42315	cyprinus ca
Q98844	anguilla an
Q7Lz75	gallus gall
P42289	xenopus lae
P42290	xenopus lae
Q98843	anguilla an
Q4riq8	tetradodon n
P53452	fugu rubrip
P42291	xenopus lae
Q91xt6	mus musculus
Q5m7u8	rattus norv
Q9d277	mus musculus
Q9u4e1	oxytricha n
Q7vm53	haemophilus
Q8L614	arabidopsis
Q8r004	mus musculus
Q8wvf1	mus musculus
Q6nuw0	brachydanio
Q99k74	mus musculus
Q4v8b3	rattus norv
O75448	h thyroid h
Q8fyk7	arabidopsis
Q54s68	dictyosteli
Q5wrx2	legionella
Q87bq8	xyella fae
Q73s32	mycobacteri
Q7rlw8	giardia lam
Q87nd8	vibrio para
P36042	saccharomyc
Q6mpa7	dbellovibri
Q6ot06	caenorhabdi
Q6k2u8	oryza sativ
Q5lq00	silicibacte
Q5fjn9	lactobacill
Q6uc26	uncultured

103	30	71.4	275	2	T12937	probable phospho	176	29	69.0	172	2	AC2548	hypothetical prote
104	30	71.4	293	2	H70067	transcription regu	177	29	69.0	185	2	E64126	hypothetical prote
105	30	71.4	301	2	A48879	urate oxidase (EC	178	29	69.0	190	2	G64065	probable methylate
106	30	71.4	302	1	A38097	urate oxidase (EC	179	29	69.0	193	2	A86852	hypothetical prote
107	30	71.4	302	2	S75921	hypothetical prote	180	29	69.0	194	2	A11038	probable exonuclea
108	30	71.4	323	2	D82241	conserved hypotet	181	29	69.0	194	2	S10629	hypothetical prote
109	30	71.4	325	2	AC0398	pseudouridylyl sy	182	29	69.0	196	2	AH1149	hypothetical prote
110	30	71.4	330	2	AB0953	asparagine synthet	183	29	69.0	205	2	A11508	hypothetical prote
111	30	71.4	330	2	F91214	asparagine synthet	184	29	69.0	208	2	AH1795	hypothetical prote
112	30	71.4	330	2	G86060	hypothetical prote	185	29	69.0	208	2	H69950	conserved hypotet
113	30	71.4	335	2	T44270	hypothetical prote	186	29	69.0	211	1	CYRTB3	beta-crystallin B3
114	30	71.4	343	2	JE0409	cellulase (EC 3.2.	187	29	69.0	211	2	B56691	mpal 5'-region hyp
115	30	71.4	343	2	JT0368	cellulase (EC 3.2.	188	29	69.0	213	2	B27898	beta-crystallin B3
116	30	71.4	354	2	AG1354	hypothetical prote	189	29	69.0	213	2	E64145	hypothetical prote
117	30	71.4	354	2	AH1724	hypothetical prote	190	29	69.0	213	2	T00938	hypothetical prote
118	30	71.4	370	2	G84042	hypothetical prote	191	29	69.0	217	2	F64657	probable glucose-6
119	30	71.4	377	2	H82022	protein T27A1.2 [i	192	29	69.0	227	2	G71859	probable dehydroge
120	30	71.4	411	2	F72494	hypothetical prote	193	29	69.0	231	2	I50467	MHC class II beta
121	30	71.4	433	2	S63143	cell division cont	194	29	69.0	232	2	H75422	probable polysacch
122	30	71.4	434	2	G82184	glycerol-3-phospha	195	29	69.0	232	2	S71935	major tegument pro
123	30	71.4	436	2	E72292	glycerol-3-phospha	196	29	69.0	248	2	S71935	probable PTS syate
124	30	71.4	438	2	E84579	hypothetical prote	197	29	69.0	259	2	C82153	probable wbb12 pro
125	30	71.4	447	2	T09414	hypothetical prote	198	29	69.0	261	2	E70723	transposase (06) B
126	30	71.4	465	2	A88868	pectinesterase nom	199	29	69.0	261	2	A84077	adenylyl-sulfate k
127	30	71.4	484	2	JE0361	protein T23B5.3 [i	200	29	69.0	276	1	S47640	nitrate transport
128	30	71.4	490	2	T25147	N-acetylglucosamin	201	29	69.0	276	1	I39928	hypothetical prote
129	30	71.4	579	2	AP2352	hypothetical prote	202	29	69.0	276	2	C86386	deoxyribonuclease
130	30	71.4	609	2	F64045	hypothetical prote	203	29	69.0	282	1	ND80A	hypothetical prote
131	30	71.4	657	2	T01301	exonuclease ABC c	204	29	69.0	291	2	S75654	Sal19R protein - v
132	30	71.4	801	2	PC6010	RNA directed DNA p	205	29	69.0	309	1	J01775	dnaJ protein homol
133	30	71.4	822	2	E86601	CHLTR probable pho	206	29	69.0	309	1	S62835	probable membrane
134	30	71.4	822	2	C72023	conserved hypotet	207	29	69.0	310	1	B64200	heat shock protein
135	30	71.4	889	2	T33422	chltr probable pho	208	29	69.0	310	1	D87506	glycosyl transfera
136	30	71.4	945	2	A64714	hypothetical prote	209	29	69.0	318	2	D87506	hypothetical prote
137	30	71.4	945	2	A64714	helicase - Helicob	210	29	69.0	326	2	T38861	UDP-glucose 4-epim
138	30	71.4	946	2	A71805	probable ATP-depen	211	29	69.0	327	2	B97076	serine/threonine-p
139	30	71.4	1036	2	S22383	axolin 1 precursor	212	29	69.0	327	2	H83659	hypothetical prote
140	30	71.4	1123	2	S36846	myosin-binding pro	213	29	69.0	332	2	T33310	hypothetical prote
141	30	71.4	1154	2	T15650	hypothetical prote	214	29	69.0	350	2	T48622	hypothetical prote
142	30	71.4	1339	2	AS5301	1,3-beta-D-glucan-	215	29	69.0	351	2	I39808	spore coat protein
143	30	71.4	1506	2	T03886	hypothetical prote	216	29	69.0	351	2	A82429	iron(III) ABC tran
144	30	71.4	1684	2	T02367	hypothetical prote	217	29	69.0	359	2	A13268	hypothetical prote
145	30	71.4	1963	1	GNVVTB	integumentary muc	218	29	69.0	364	2	T43467	hypothetical prote
146	30	71.4	2264	1	GNVVTB	genome polyprotein	219	29	69.0	373	2	T10341	late expression fa
147	30	71.4	2481	2	A43908	myosin heavy chain	220	29	69.0	381	2	S60561	I kappa B-like pro
148	30	71.4	2911	2	T20566	fibronectin - Afri	221	29	69.0	386	2	S72168	dopamine receptor
149	30	71.4	5107	2	T29144	hypothetical prote	222	29	69.0	387	2	T32929	3-oxoacyl-acyl-ca
150	30	71.4	26926	1	G36852	partial CDS - Caen	223	29	69.0	388	2	AG3341	hypothetical prote
151	29	69.0	74	1	G36852	titin, cardiac mus	224	29	69.0	398	2	S17428	ATP-gated ion chan
152	29	69.0	74	2	B72169	hypothetical prote	225	29	69.0	401	2	T42655	interleukin-1 rece
153	29	69.0	76	2	AB0648	A45R protein - var	226	29	69.0	403	2	S57646	hypothetical prote
154	29	69.0	76	2	AB0648	cation transport r	227	29	69.0	403	2	B87513	acyl-CoA dehydroge
155	29	69.0	76	2	AB5702	cation transport r	228	29	69.0	403	2	E43521	A39R protein - vac
156	29	69.0	76	2	F64868	cation transport r	229	29	69.0	421	2	T14773	hypothetical prote
157	29	69.0	81	2	T37233	hypothetical prote	230	29	69.0	423	2	B64079	probable amidohydr
158	29	69.0	81	2	A95908	conserved hypotet	231	29	69.0	433	2	T51533	hypothetical prote
159	29	69.0	94	2	AC1474	hypothetical prote	232	29	69.0	435	2	F82821	NADH-ubiquinone ox
160	29	69.0	102	2	S50530	hypothetical prote	233	29	69.0	435	2	T05452	hypothetical prote
161	29	69.0	108	2	JQ2202	hypothetical prote	234	29	69.0	441	2	S29921	hypothetical prote
162	29	69.0	108	2	S21420	hypothetical 12.6K	235	29	69.0	448	2	C64437	probable urease
163	29	69.0	112	2	A45069	general stress pro	236	29	69.0	472	2	H96607	unknown protein F2
164	29	69.0	122	2	AD1092	omega-agatoxin IA	237	29	69.0	473	2	E64120	exodoxyribonuclea
165	29	69.0	122	2	AC1456	hypothetical prote	238	29	69.0	482	2	E70450	UDP-MurNac-tripept
166	29	69.0	132	2	AC1382	hypothetical prote	239	29	69.0	482	2	T36146	cytochrome P450, C
167	29	69.0	132	2	AB1752	hypothetical prote	240	29	69.0	485	1	JC5236	E2 protein - human
168	29	69.0	134	2	JQ1355	V0 protein - Miasa	241	29	69.0	498	1	W2ML8	E2 protein - human
169	29	69.0	139	2	T49524	hypothetical prote	242	29	69.0	502	2	S36494	hypothetical prote
170	29	69.0	141	2	B81219	hypothetical prote	243	29	69.0	510	2	T16146	hypothetical prote
171	29	69.0	146	2	S10089	beta-crystallin B3	244	29	69.0	511	1	PC4054	cardiac C-protein
172	29	69.0	149	2	T25858	hypothetical prote	245	29	69.0	511	1	S25707	cytochrome P450 4D
173	29	69.0	158	2	S49918	hypothetical prote	246	29	69.0	512	2	E90600	hypothetical prote
174	29	69.0	158	2	AD3583	riboflavin synthas	247	29	69.0	514	1	T13611	hypothetical prote
175	29	69.0	171	2	AI0227	hypothetical prote	248	29	69.0	514	1	W2ML5	E2 protein - human

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 11.6667 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-12

Perfect score: 42

Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	92.9	363	2 I50475	dopamine D1 recept
2	38	90.5	240	2 E97002	fusion: transcript
3	37	88.1	238	2 B75033	hypothetical prote
4	36	85.7	428	2 T21450	hypothetical prote
5	35	83.3	204	2 A44583	venom allergen ant
6	35	83.3	204	2 B44583	venom allergen ant
7	35	83.3	961	2 A82270	exonuclease ABC c
8	35	83.3	1666	2 T43169	hypothetical prote
9	34	81.0	247	2 A96932	phosphoserine phos
10	34	81.0	320	2 A13234	hypothetical prote
11	34	81.0	429	2 H71539	probable dihydrol
12	34	81.0	446	1 DXHUD1	dopamine receptor
13	34	81.0	446	2 I47217	dopamine receptor
14	34	81.0	450	2 A55886	dopamine receptor
15	34	81.0	451	2 I51659	dopamine D1A recep
16	34	81.0	457	2 I51660	dopamine D1B recep
17	34	81.0	459	2 A56849	dopamine receptor-
18	34	81.0	465	2 I51661	dopamine D1C recep
19	34	81.0	487	1 DXRDT1	dopamine receptor
20	33	78.6	193	2 S38039	hypothetical prote
21	33	78.6	348	2 T11141	NADH2 dehydrogenas
22	33	78.6	444	2 C55886	dopamine receptor
23	33	78.6	466	1 B43332	glutamate decarbox
24	33	78.6	466	1 S42334	glutamate decarbox
25	33	78.6	466	1 E91178	glutamate decarbox
26	33	78.6	466	2 F86024	glutamate decarbox
27	33	78.6	466	2 G85726	glutamate decarbox
28	33	78.6	466	2 B90891	glutamate decarbox
29	33	78.6	1898	2 T42440	phospholipase C ho

30	33	78.6	1922	2 T21581	hypothetical prote
31	32	76.2	49	2 S72972	hypothetical prote
32	32	76.2	100	2 B70977	probable secreted
33	32	76.2	104	2 C86954	hypothetical prote
34	32	76.2	108	2 C71644	hypothetical prote
35	32	76.2	124	2 AH1238	hypothetical prote
36	32	76.2	197	2 S19102	CS6 subunits chape
37	32	76.2	232	1 I83349	translocation prot
38	32	76.2	307	2 A36955	protein C50H11.9 [
39	32	76.2	353	2 H88985	CPGlucoase 4,6-deh
40	32	76.2	359	2 AH0766	rfbg protein - Sal
41	32	76.2	359	2 S15305	hypothetical prote
42	32	76.2	383	2 T39854	mannose-1-phosphat
43	32	76.2	389	2 A12230	heterocyst envelop
44	32	76.2	389	2 AC2268	hypothetical prote
45	32	76.2	409	2 S77262	probable transport
46	32	76.2	411	2 B82246	diacylglycerol S
47	32	76.2	420	2 D84965	pyruvate dehydroge
48	32	76.2	428	2 F81694	dihydrolipoamide a
49	32	76.2	429	2 B86529	pyruvate dehydroge
50	32	76.2	429	2 B72095	small chain of NAD
51	32	76.2	479	2 B97106	hypothetical prote
52	32	76.2	511	2 S53051	probable chromatin
53	32	76.2	512	2 T38422	hypothetical prote
54	32	76.2	905	2 S29329	probable C2H2-type
55	32	76.2	907	2 T02417	hypothetical prote
56	32	76.2	1449	2 B84426	hypothetical prote
57	32	76.2	1555	2 T18688	protein B0272.5 [i
58	32	76.2	1973	2 G89608	hypothetical prote
59	32	76.2	1973	2 T18686	B. subtilis Yaal P
60	31	73.8	80	2 AC1788	dopamine receptor
61	31	73.8	156	2 I67751	dopamine receptor
62	31	73.8	161	2 A48909	venom allergen ant
63	31	73.8	204	2 C44583	lipopolysaccharide
64	31	73.8	265	2 AD0972	zfaP protein - Esc
65	31	73.8	265	2 C42595	aspartate-ammonia
66	31	73.8	330	2 D95230	aspartate-ammonia
67	31	73.8	332	2 G98094	hypothetical prote
68	31	73.8	389	2 C96603	probable major tai
69	31	73.8	390	2 AD1035	neuroblast cell li
70	31	73.8	417	2 A49129	UDP-N-acetylmuramo
71	31	73.8	455	2 AD1329	UDP-N-acetylmuramo
72	31	73.8	455	2 AD1700	dopamine receptor-
73	31	73.8	463	2 B56849	dopamine receptor
74	31	73.8	475	2 A41271	dopamine receptor
75	31	73.8	477	1 DXHUD5	dopamine receptor
76	31	73.8	486	2 B55886	hypothetical prote
77	31	73.8	501	2 T28970	hypothetical prote
78	31	73.8	505	2 S54066	hypothetical prote
79	31	73.8	521	2 T46250	hypothetical prote
80	31	73.8	521	2 T38454	methionine-tRNA li
81	31	73.8	539	2 G64616	penta-phosphate gu
82	31	73.8	775	2 C71898	guanosine-3',5'-bi
83	31	73.8	799	2 JH0797	castor protein - f
84	31	73.8	803	1 A64070	endopeptidase La (
85	31	73.8	824	2 AD3098	periplasmic nitrat
86	31	73.8	834	2 E98188	periplasmic nitrat
87	31	73.8	894	2 F69730	cell wall-associat
88	31	73.8	900	2 T33482	hypothetical prote
89	31	73.8	1062	2 H83966	carbamoyl-phosphat
90	31	73.8	2518	2 A12140	polyketide synthas
91	31	73.8	3707	2 S18252	heparan sulfate pr
92	31	73.8	4391	2 A38096	protein UNC-89 - C
93	31	73.8	6642	2 T29757	hypothetical prote
94	30	71.4	92	2 G82566	pyruvate ferredoxi
95	30	71.4	186	2 F71857	pyruvate ferredoxi
96	30	71.4	204	2 B46458	antigen 5 - easter
97	30	71.4	204	2 B37329	hypothetical prote
98	30	71.4	210	2 B81343	hypothetical prote
99	30	71.4	245	2 T19657	hypothetical prote
100	30	71.4	247	2 T49375	hypothetical prote
101	30	71.4	264	2 G96978	uncharacterized co
102	30	71.4	272	2 H83269	hypothetical prote

98	32	76.2	108	5	ABP66786	Human pol	171	31	73.8	265	9	AEA03059	AEA03059	Lipid A b
99	32	76.2	108	7	ADB31669	Human nov	172	31	73.8	266	7	ADC32794	ADC32794	Human nov
100	32	76.2	116	4	AAU57695	Propionib	173	31	73.8	267	8	ADR50904	ADR50904	Protein d
101	32	76.2	116	5	ABM54214	Propionib	174	31	73.8	327	8	ABU02474	ABU02474	S. pneumo
102	32	76.2	124	5	ABM48097	Listeria	175	31	73.8	330	8	ADK47108	ADK47108	Streptoco
103	32	76.2	125	5	ABP32249	Human nuc	176	31	73.8	330	8	ADM92240	ADM92240	S. pneumo
104	32	76.2	155	4	AAU06762	Human fce	177	31	73.8	332	6	ABP81644	ABP81644	Streptoco
105	32	76.2	160	6	ABM69532	Photorhab	178	31	73.8	355	7	ADC86179	ADC86179	Human GPC
106	32	76.2	212	6	ADR14914	Escherich	179	31	73.8	394	2	AAW26726	AAW26726	Human int
107	32	76.2	230	6	ABU40121	Protein e	180	31	73.8	394	2	AAW26928	AAW26928	Human int
108	32	76.2	326	3	ADN27151	Bacterial	181	31	73.8	394	2	AAE00737	AAE00737	Human int
109	32	76.2	332	3	AAU34831	Gene 27 h	182	31	73.8	394	4	AAU00737	AAU00737	Human int
110	32	76.2	359	2	AAW88341	Salmonell	183	31	73.8	394	6	ABM32681	ABM32681	Human cyt
111	32	76.2	393	3	AAU27624	Human sec	184	31	73.8	394	6	ABU62800	ABU62800	Human int
112	32	76.2	393	4	AAU01974	Gene #12	185	31	73.8	394	8	ADO20109	ADO20109	Human PRO
113	32	76.2	393	4	AAU060757	Gene 12 r	186	31	73.8	394	8	ADP54948	ADP54948	Human PRO
114	32	76.2	393	4	AAU060757	Gene 12 r	187	31	73.8	394	8	ADR97372	ADR97372	Human PRO
115	32	76.2	432	3	AAU34903	Chlamydia	188	31	73.8	394	9	ADY17560	ADY17560	PRO poly
116	32	76.2	438	6	ABU24541	Protein e	189	31	73.8	416	5	ABU51616	ABU51616	Helicobac
117	32	76.2	479	6	ABU23870	Protein e	190	31	73.8	425	5	ADQ67079	ADQ67079	Novel hum
118	32	76.2	479	7	ADP04571	Bacterial	191	31	73.8	426	8	ABU48473	ABU48473	Listeria
119	32	76.2	486	8	ADS51620	Arabidops	192	31	73.8	455	5	ABU32621	ABU32621	Protein e
120	32	76.2	511	5	AAU82963	S. cerevi	193	31	73.8	455	6	ABU18927	ABU18927	Protein e
121	32	76.2	511	8	ADN19235	Bacterial	194	31	73.8	458	6	ADV89674	ADV89674	Streptoco
122	32	76.2	590	8	ADS51622	Soybean C	195	31	73.8	466	8	ADV83075	ADV83075	Streptoco
123	32	76.2	614	8	ADS21284	Bacterial	196	31	73.8	466	8	ADH69508	ADH69508	Rat D18 d
124	32	76.2	661	2	AAW77048	Human str	197	31	73.8	475	2	AAU31046	AAU31046	Streptoco
125	32	76.2	661	3	AAU70078	Human str	198	31	73.8	475	8	ADH69508	ADH69508	Rat D18 d
126	32	76.2	928	8	ADY04709	Plant ful	199	31	73.8	475	8	ADO29017	ADO29017	Mouse nov
127	32	76.2	1449	8	ADJ50120	Oil-associ	200	31	73.8	475	8	AAU21082	AAU21082	Dopamine
128	32	76.2	1902	4	ABE65387	Drosophil	201	31	73.8	477	2	AAU79381	AAU79381	Dopamine
129	32	76.2	3186	7	ADJ78942	Human NOV	202	31	73.8	477	2	AAU40802	AAU40802	Human D5
130	32	76.2	3186	8	ADJ78942	Human NOV	203	31	73.8	477	4	ABM56350	ABM56350	Non-endog
131	32	76.2	3208	7	ADJ78942	Human NOV	204	31	73.8	477	6	ABP81808	ABP81808	Human dop
132	32	76.2	3208	8	ADJ78946	Human NOV	205	31	73.8	477	7	ADK52546	ADK52546	Hematolog
133	32	76.2	3252	8	ADJ78944	Human NOV	206	31	73.8	477	8	ADH69494	ADH69494	Human dop
134	32	76.2	3252	8	ADJ78944	Human NOV	207	31	73.8	477	8	ADH69494	ADH69494	Human dop
135	32	76.2	3267	7	ADP99075	Human KPP	208	31	73.8	477	8	ADO29016	ADO29016	Human nov
136	32	76.2	3267	7	ADP99075	Human KPP	209	31	73.8	477	8	ADH73655	ADH73655	Human nov
137	32	76.2	36946	9	ADV97835	Murine pr	210	31	73.8	478	9	AEA55027	AEA55027	Mouse D(1
138	31	73.8	41	5	ABJ05469	Human bre	211	31	73.8	478	9	AEA55027	AEA55027	Mouse D(1
139	31	73.8	51	6	ABP78415	N. gonorr	212	31	73.8	479	2	AAU22546	AAU22546	Truncated
140	31	73.8	62	5	ABP05202	Human ORF	213	31	73.8	479	2	AAU22546	AAU22546	Truncated
141	31	73.8	64	4	AAU90119	Human imm	214	31	73.8	480	5	ABG78365	ABG78365	Human pro
142	31	73.8	68	4	AAU16885	Peptide #	215	31	73.8	480	5	ABG78365	ABG78365	Human pro
143	31	73.8	68	4	ABM35866	Peptide #	216	31	73.8	488	5	ADQ90948	ADQ90948	Human 9-0
144	31	73.8	68	4	ABM35866	Peptide #	217	31	73.8	488	5	ADQ90948	ADQ90948	Human 9-0
145	31	73.8	68	4	ABM35866	Peptide #	218	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
146	31	73.8	68	4	ABM35866	Peptide #	219	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
147	31	73.8	68	4	ABM35866	Peptide #	220	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
148	31	73.8	68	4	ABM35866	Peptide #	221	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
149	31	73.8	68	4	ABM35866	Peptide #	222	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
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153	31	73.8	128	6	AAU01086	Gene 9 Hu	226	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
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156	31	73.8	144	4	AAU74424	Plant ful	229	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
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167	31	73.8	257	4	ABM59453	Drosophil	240	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
168	31	73.8	257	8	ADX80047	Plant ful	241	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
169	31	73.8	265	6	ABU79128	Lipid A b	242	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0
170	31	73.8	265	7	ADF43388	Lipid A b	243	31	73.8	488	7	ADQ90948	ADQ90948	Human 9-0

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 61.5417 Seconds

(without alignments)

49.977 Million cell updates/sec

Title: US-10-091-135-12

Perfect score: 42

Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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5: geneseqp2002s.*

6: geneseqp2003as.*

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8: geneseqp2004s.*

9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	42	100.0	7	AAE28818	Aae28818 Vesputia v
2	37	88.1	238	AAE96339	Aae96339 Putative
3	36	85.7	170	ADH88291	Adh88291 Plant ful
4	36	85.7	222	ADH93307	Adh93307 Plant ful
5	36	85.7	513	ABU20705	Abu20705 Protein e
6	35	83.3	20	AAW35678	Aaw35678 T cell pe
7	35	83.3	49	AAE28814	Aae28814 Vesputia v
8	35	83.3	204	AAW35688	Aaw35688 Vesputia v
9	35	83.3	204	AAW45217	Aaw45217 Wild type
10	35	83.3	204	ABG66977	Abg66977 Wasp veno
11	35	83.3	204	ABG66983	Abg66983 Wasp veno
12	35	83.3	204	ABG67052	Abg67052 Wasp veno
13	35	83.3	204	ABG67104	Abg67104 Wasp veno
14	35	83.3	204	ABG67103	Abg67103 Wasp veno
15	35	83.3	204	ABG67103	Abg67103 Wasp veno
16	35	83.3	209	ABM00031	Abm00031 Allergen
17	35	83.3	227	AAE25644	Aae25644 Vesputia v
18	35	83.3	227	AAE13071	Aae13071 Vesputia v
19	35	83.3	227	AAW34893	Aaw34893 Wasp alle
20	35	83.3	316	AAW29651	Aaw29651 Human sec
21	35	83.3	503	ABU11748	Abu11748 Human MDD
22	35	83.3	748	ADH74313	Adh74313 PRO polyp
23	35	83.3	804	ABU39533	Abu39533 Protein e
24	35	83.3	1060	AAW79933	Aaw79933 CGDD-8, I

99	29	58.0	283	7	US-11-096-568A-33613	Sequence 33613, A	172	28	56.0	166	7	US-11-132-722-13	Sequence 13, Appl
100	29	58.0	286	7	US-11-172-740-1944	Sequence 1944, Ap	173	28	56.0	166	7	US-11-132-722-14	Sequence 14, Appl
101	29	58.0	287	7	US-11-188-298-1321	Sequence 1321, A	174	28	56.0	166	7	US-11-132-722-15	Sequence 15, Appl
102	29	58.0	287	7	US-11-096-568A-33436	Sequence 33436, A	175	28	56.0	166	7	US-11-132-722-16	Sequence 16, Appl
103	29	58.0	287	7	US-11-188-298-373	Sequence 373, App	176	28	56.0	166	7	US-11-132-722-17	Sequence 17, Appl
104	29	58.0	287	7	US-11-188-298-678	Sequence 678, App	177	28	56.0	166	7	US-11-132-722-18	Sequence 18, Appl
105	29	58.0	304	7	US-11-096-568A-7821	Sequence 7821, Ap	178	28	56.0	166	7	US-11-132-722-19	Sequence 19, Appl
106	29	58.0	317	7	US-11-188-298-3143	Sequence 3143, Ap	179	28	56.0	166	7	US-11-132-722-20	Sequence 20, Appl
107	29	58.0	327	7	US-11-096-568A-16686	Sequence 16686, A	180	28	56.0	166	7	US-11-132-722-21	Sequence 21, Appl
108	29	58.0	359	7	US-11-188-298-14325	Sequence 14325, A	181	28	56.0	166	7	US-11-132-722-22	Sequence 22, Appl
109	29	58.0	359	7	US-11-188-298-15537	Sequence 15537, A	182	28	56.0	166	7	US-11-132-722-23	Sequence 23, Appl
110	29	58.0	360	7	US-11-108-528-8	Sequence 8, Appli	183	28	56.0	166	7	US-11-132-722-24	Sequence 24, Appl
111	29	58.0	364	7	US-11-096-568A-7820	Sequence 7820, Ap	184	28	56.0	166	7	US-11-132-722-25	Sequence 25, Appl
112	29	58.0	379	7	US-11-096-568A-10207	Sequence 10207, A	185	28	56.0	166	7	US-11-132-722-26	Sequence 26, Appl
113	29	58.0	385	7	US-11-096-568A-31309	Sequence 31309, A	186	28	56.0	166	7	US-11-132-722-27	Sequence 27, Appl
114	29	58.0	393	6	US-10-527-500-7	Sequence 7, Appli	187	28	56.0	166	7	US-11-132-722-28	Sequence 28, Appl
115	29	58.0	400	7	US-11-098-686-10428	Sequence 10428, A	188	28	56.0	166	7	US-11-132-722-29	Sequence 29, Appl
116	29	58.0	412	7	US-11-079-463-8276	Sequence 8276, Ap	189	28	56.0	166	7	US-11-132-722-30	Sequence 30, Appl
117	29	58.0	424	7	US-11-096-568A-31308	Sequence 31308, A	190	28	56.0	166	7	US-11-132-722-31	Sequence 31, Appl
118	29	58.0	429	7	US-11-096-568A-854	Sequence 854, App	191	28	56.0	166	7	US-11-132-722-32	Sequence 32, Appl
119	29	58.0	459	7	US-11-096-568A-31307	Sequence 31307, A	192	28	56.0	166	7	US-11-132-722-33	Sequence 33, Appl
120	29	58.0	480	7	US-11-096-568A-31201	Sequence 31201, A	193	28	56.0	166	7	US-11-132-722-34	Sequence 34, Appl
121	29	58.0	505	7	US-11-096-568A-853	Sequence 853, App	194	28	56.0	166	7	US-11-132-722-35	Sequence 35, Appl
122	29	58.0	513	7	US-11-096-568A-31200	Sequence 31200, A	195	28	56.0	166	7	US-11-132-722-36	Sequence 36, Appl
123	29	58.0	518	7	US-11-096-568A-852	Sequence 852, App	196	28	56.0	166	7	US-11-132-722-37	Sequence 37, Appl
124	29	58.0	519	7	US-11-096-568A-31199	Sequence 31199, A	197	28	56.0	166	7	US-11-132-722-38	Sequence 38, Appl
125	29	58.0	531	7	US-11-072-512-3442	Sequence 3442, Ap	198	28	56.0	166	7	US-11-132-722-39	Sequence 39, Appl
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128	29	58.0	627	7	US-11-096-568A-29899	Sequence 29899, A	201	28	56.0	166	7	US-11-132-722-42	Sequence 42, Appl
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131	29	58.0	644	7	US-11-024-959-411	Sequence 411, App	204	28	56.0	166	7	US-11-132-722-45	Sequence 45, Appl
132	29	58.0	693	7	US-11-167-856-2	Sequence 2, Appli	205	28	56.0	166	7	US-11-132-722-46	Sequence 46, Appl
133	29	58.0	780	7	US-11-096-568A-29956	Sequence 29956, A	206	28	56.0	166	7	US-11-132-722-47	Sequence 47, Appl
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135	29	58.0	838	7	US-11-096-568A-29954	Sequence 29954, A	208	28	56.0	166	7	US-11-132-722-49	Sequence 49, Appl
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137	29	58.0	858	7	US-11-188-298-8992	Sequence 8992, Ap	210	28	56.0	166	7	US-11-132-722-51	Sequence 51, Appl
138	29	58.0	872	7	US-11-096-568A-18658	Sequence 18658, A	211	28	56.0	166	7	US-11-132-722-52	Sequence 52, Appl
139	29	58.0	948	6	US-11-241-956-10	Sequence 10, Appl	212	28	56.0	167	7	US-11-077-813A-2	Sequence 2, Appli
140	29	58.0	963	6	US-10-467-962B-2	Sequence 2, Appli	213	28	56.0	167	7	US-11-077-813A-15	Sequence 15, Appl
141	29	58.0	1005	7	US-11-080-991-90	Sequence 90, Appl	214	28	56.0	168	7	US-11-108-298-5987	Sequence 5987, Ap
142	29	58.0	1417	7	US-11-052-554A-8	Sequence 8, Appli	215	28	56.0	181	7	US-11-147-493-6	Sequence 6, Appli
143	29	58.0	1562	7	US-11-052-554A-211	Sequence 211, App	216	28	56.0	189	7	US-11-147-493-12	Sequence 12, Appl
144	28	57.0	668	7	US-10-467-657-8775	Sequence 8775, Ap	217	28	56.0	189	7	US-11-147-493-14	Sequence 14, Appl
145	28	56.0	19	6	US-10-532-153-35	Sequence 35, App	218	28	56.0	189	7	US-11-147-492-20	Sequence 20, Appl
146	28	56.0	35	6	US-10-995-561-591	Sequence 591, App	219	28	56.0	189	7	US-11-147-492-22	Sequence 22, Appl
147	28	56.0	76	6	US-10-995-561-592	Sequence 592, App	220	28	56.0	189	7	US-11-147-492-24	Sequence 24, Appl
148	28	56.0	102	7	US-11-079-463-8109	Sequence 8109, Ap	221	28	56.0	189	7	US-11-147-492-28	Sequence 28, Appl
149	28	56.0	105	7	US-11-087-099-7998	Sequence 7998, Ap	222	28	56.0	189	7	US-11-147-493-30	Sequence 30, Appl
150	28	56.0	109	7	US-11-188-298-4889	Sequence 4889, Ap	223	28	56.0	201	7	US-11-096-568A-25909	Sequence 25909, A
151	28	56.0	120	7	US-11-077-813A-4	Sequence 4, Appli	224	28	56.0	212	6	US-10-947-071-5	Sequence 5, Appli
152	28	56.0	127	6	US-10-467-657-5606	Sequence 5606, Ap	225	28	56.0	212	6	US-10-948-097-5	Sequence 5, Appli
153	28	56.0	137	6	US-11-072-512-3241	Sequence 3241, Ap	226	28	56.0	213	6	US-10-467-657-5338	Sequence 5338, Ap
154	28	56.0	148	6	US-10-484-516-5	Sequence 6, Appli	227	28	56.0	220	7	US-11-096-568A-25908	Sequence 25908, A
155	28	56.0	148	6	US-10-484-516-6	Sequence 6, Appli	228	28	56.0	220	7	US-10-714-887-184	Sequence 184, App
156	28	56.0	159	6	US-10-484-516-4	Sequence 4, Appli	229	28	56.0	228	7	US-11-096-568A-25907	Sequence 25907, A
157	28	56.0	160	6	US-11-176-830-232	Sequence 232, App	230	28	56.0	239	6	US-10-980-388-76	Sequence 76, Appl
158	28	56.0	165	7	US-11-132-722-1	Sequence 1, Appli	231	28	56.0	259	7	US-11-188-298-9214	Sequence 9214, Ap
159	28	56.0	166	7	US-11-132-722-2	Sequence 2, Appli	232	28	56.0	259	7	US-11-188-298-8982	Sequence 8982, Ap
160	28	56.0	166	7	US-11-132-722-3	Sequence 3, Appli	233	28	56.0	260	7	US-11-188-298-16871	Sequence 16871, A
161	28	56.0	166	7	US-11-132-722-4	Sequence 4, Appli	234	28	56.0	267	7	US-11-188-298-9273	Sequence 9273, Ap
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163	28	56.0	166	7	US-11-132-722-6	Sequence 6, Appli	236	28	56.0	273	7	US-11-188-298-7098	Sequence 7098, App
164	28	56.0	166	7	US-11-132-722-7	Sequence 7, Appli	237	28	56.0	277	7	US-11-188-298-3698	Sequence 3698, Ap
165	28	56.0	166	7	US-11-132-722-8	Sequence 8, Appli	238	28	56.0	290	7	US-11-096-568A-19725	Sequence 19725, A
166	28	56.0	166	7	US-11-132-722-9	Sequence 9, Appli	239	28	56.0	290	7	US-11-123-013-2	Sequence 2, Appli
167	28	56.0	166	7	US-11-132-722-10	Sequence 10, Appl	240	28	56.0	304	7	US-11-124-368A-201	Sequence 201, App
168	28	56.0	166	7	US-11-132-722-11	Sequence 11, Appl	241	28	56.0	311	7	US-11-124-368A-206	Sequence 206, App
169	28	56.0	166	7	US-11-132-722-12	Sequence 12, Appl	242	28	56.0	311	7		
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:28:47 ; Search time 8.25 Seconds
(without alignments)
46.352 Million cell updates/sec

Title: US-10-091-135-11

Perfect score: 50

Sequence: 1 PKKFSQND 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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3	34	68.0	184	7	US-11-188-298-18036
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:24:04 ; Search time 12.5625 Seconds
59.230 Million cell updates/sec
(without alignments)

Title: US-10-091-135-11
Perfect score: 50
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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	37	74.0	25	1	US-08-614-935-68
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108	35	70.0	588	2	Q9NCM2_PLAVI	Q9ncm2 plasmodium	181	34	68.0	678	2	Q54HJ2_DICDI	Q54HJ2 dictyosteli
109	35	70.0	588	2	Q9NCM4_PLAVI	Q9ncm4 plasmodium	182	34	68.0	684	2	Q4IAU9_GIBZE	Q4IAU9 gibberella
110	35	70.0	597	2	Q4W444_HORSE	Q4W444 equus caball	183	34	68.0	686	2	Q7KITV_DROME	Q7KITV drosophila
111	35	70.0	599	2	Q9NCN2_PLAVI	Q9ncn2 plasmodium	184	34	68.0	701	2	Q7MMQ1_PORGI	Q7MMQ1 porphyromon
112	35	70.0	599	2	Q9NCM5_PLAVI	Q9ncm5 plasmodium	185	34	68.0	720	2	Q7Z2C9_DROME	Q7Z2C9 drosophila
113	35	70.0	614	2	Q9NCM9_PLAVI	Q9ncm9 plasmodium	186	34	68.0	720	2	Q9VNX6_DROME	Q9VNX6 arabisopsis
114	35	70.0	627	2	Q938J9_SCAUD	Q938J9 temperate p	187	34	68.0	770	2	Q9MA85_ARATH	Q9MA85 rattus norv
115	35	70.0	627	2	Q79X11_STRF3	Q79X11 streptococc	188	34	68.0	776	1	ZCC2_RAT	ZCC2 rat
116	35	70.0	627	2	Q8K795_STRP3	Q8K795 streptococc	189	34	68.0	776	2	Q5QUM6_IDILO	Q5QUM6 idiomatica
117	35	70.0	685	1	SNWA_DICDI	P54210 dictyosteli	190	34	68.0	784	2	Q6C3M0_YARLI	Q6C3M0 yarrowia li
118	35	70.0	695	2	Q5SDS2_DICDI	Q5SDs2 dictyosteli	191	34	68.0	787	2	Q72UQ4_LEPIC	Q72UQ4 leptospira
119	35	70.0	730	2	Q8PN69_XANAC	Q8PN69 xanthomonas	192	34	68.0	787	2	Q8F093_LEPIN	Q8F093 leptospira
120	35	70.0	736	2	Q65AC2_HORSE	Q65ac2 equus caball	193	34	68.0	939	2	Q4I181_GIBZE	Q4I181 gibberella
121	35	70.0	747	2	Q5GX84_XANON	Q5GX84 xanthomonas	194	34	68.0	981	2	Q61ZP7_CAEBR	Q61ZP7 caenorhabdi
122	35	70.0	777	2	Q4URY5_XANCP	Q4URY5 xanthomonas	195	34	68.0	1038	2	Q5B8E3_EMENI	Q5B8E2 aspergillus
123	35	70.0	777	2	Q8PBL4_XANCP	Q8PBL4 xanthomonas	196	34	68.0	1042	2	Q54L51_DICDI	Q54L51 dictyosteli
124	35	70.0	931	2	Q4JVF0_CORJK	Q4JVF0 corynebacte	197	34	68.0	1064	2	Q4WYR4_ASEFU	Q4WYR4 aspergillus
125	35	70.0	997	2	Q4PGY8_USTWA	Q4PGY8 ustilago ma	198	34	68.0	1222	2	Q54YC4_DICDI	Q54YC4 dictyosteli
126	35	70.0	1017	2	Q44055_STYLE	Q44055 stylonychia	199	34	68.0	1619	2	Q13407_MAGGR	Q13407 magnaporthe
127	35	70.0	1036	2	Q6P9K7_MOUSE	Q6P9K7 mus musculus	200	34	68.0	1633	2	Q5CXY0_CRYPV	Q5CXY0 cryptospori
128	35	70.0	1103	1	PMAL_DUNAC	P54210 dunaliella	201	34	68.0	1803	2	Q7RKR5_PLAYO	Q7RKR5 plasmodium
129	35	70.0	1134	2	Q9NPG3_HUMAN	Q9NPG3 homo sapien	202	34	68.0	2057	2	Q7R4F0_GIALA	Q7R4F0 giardia lam
130	35	70.0	1134	2	Q9P1P7_HUMAN	Q9P1P7 homo sapien	203	33	66.0	42	2	P79052_SCHPO	P79052 schizosacch
131	35	70.0	1134	2	Q4GPF8_MOUSE	Q4GPF8 mus musculus	204	33	66.0	67	2	Q5QN96_ORYSA	Q5QN96 oryza sativ
132	35	70.0	1431	1	HEXAP_HUMAN	Q96T23 homo sapien	205	33	66.0	73	2	Q64S88_BACFR	Q64S88 bacteroides
133	35	70.0	1480	2	Q9SB63_ARATH	Q9SB63 arabisopsis	206	33	66.0	80	2	Q5JYN9_ORYSA	Q5JYN9 oryza sativ
134	35	70.0	1699	2	Q81IK9_PLAVI	Q81IK9 plasmodium	207	33	66.0	87	2	Q7RT83_PLAYO	Q7RT83 plasmodium
135	35	70.0	1708	2	Q81IK6_PLAVI	Q81IK6 plasmodium	208	33	66.0	109	2	Q5VR42_ORYSA	Q5VR42 oryza sativ
136	35	70.0	1716	2	Q81IM2_PLAVI	Q81IM2 plasmodium	209	33	66.0	111	1	CYC2_AGRIC	CYC2 agrobacteri
137	35	70.0	1716	2	Q81OK3_PLAVI	Q81OK3 plasmodium	210	33	66.0	112	2	Q6Z6T1_ORYSA	Q6Z6T1 oryza sativ
138	35	70.0	1721	2	Q81IM3_PLAVI	Q81IM3 plasmodium	211	33	66.0	139	2	Q8U7S0_AGR5	Q8U7S0 agrobacteri
139	35	70.0	1731	2	Q81IL3_PLAVI	Q81IL3 plasmodium	212	33	66.0	190	2	Q8LD03_ARATH	Q8LD03 arabisopsis
140	35	70.0	1739	2	Q81IL8_PLAVI	Q81IL8 plasmodium	213	33	66.0	190	2	Q9LF15_ARATH	Q9LF15 arabisopsis
141	35	70.0	1742	2	Q81IL4_PLAVI	Q81IL4 plasmodium	214	33	66.0	190	2	Q9KF29_BACHD	Q9KF29 bacillus ha
142	35	70.0	1749	2	Q81IL7_PLAVI	Q81IL7 plasmodium	215	33	66.0	191	2	Q9CS14_ARATH	Q9CS14 arabisopsis
143	35	70.0	1751	2	Q81OG9_PLAVI	Q81OG9 plasmodium	216	33	66.0	191	2	Q9M885_ARATH	Q9M885 arabisopsis
144	35	70.0	1751	2	Q26194_PLAVI	Q26194 plasmodium	217	33	66.0	192	1	RS7_ORYSA	RS7 oryza sativ
145	35	70.0	1756	2	Q81IM1_PLAVI	Q81IM1 plasmodium	218	33	66.0	192	1	RS7_SECC	RS7 secale cere
146	35	70.0	1756	2	Q81O58_PLAVI	Q81O58 plasmodium	219	33	66.0	192	2	Q5W6R3_ORYSA	Q5W6R3 oryza sativ
147	35	70.0	1761	2	Q81O91_PLAVI	Q81O91 plasmodium	220	33	66.0	192	2	Q6Z786_ORYSA	Q6Z786 oryza sativ
148	35	70.0	1763	2	Q81IL2_PLAVI	Q81IL2 plasmodium	221	33	66.0	205	2	Q9JKC5_MOUSE	Q9JKC5 mus musculu
149	35	70.0	2228	2	Q7RG88_PLAYO	Q7RG88 mycoplasma	222	33	66.0	210	2	Q8WVB8_IXOSC	Q8WVB8 ixodes scap
150	35	68.0	84	2	Q60B22_MYCHY	Q60B22 mycoplasma	223	33	66.0	220	2	Q68V26_MOUSE	Q68V26 mus musculu
151	34	68.0	107	2	Q6MB72_PAROW	Q6MB72 parachlamyd	224	33	66.0	220	2	Q68V27_MOUSE	Q68V27 mus musculu
152	34	68.0	134	2	Q72V43_LEPIC	Q72V43 leptospira	225	33	66.0	220	2	Q4XE72_PLACH	Q4XE72 plasmodium
153	34	68.0	134	2	Q8CXR5_LEPIN	Q8CXr5 leptospira	226	33	66.0	234	2	Q8C1Q8_MOUSE	Q8C1Q8 mus musculu
154	34	68.0	145	2	Q661C3_BORGA	Q661C3 borrelia ga	227	33	66.0	249	2	Q61E63_RAT	Q61E63 rattus norv
155	34	68.0	221	2	Q8GQX1_SELRU	Q8GQX1 selenomonas	228	33	66.0	249	2	Q7Q9W5_ANOGA	Q7Q9W5 anopheles g
156	34	68.0	263	2	Q4SLJ1_TETNG	Q4SLJ1 tetraodon n	229	33	66.0	288	2	Q6Z5D1_CAEBR	Q6Z5D1 caenorhabdi
157	34	68.0	266	2	Q48894_MICAE	Q48894 microcystis	230	33	66.0	291	2	Q6YU39_ORYSA	Q6YU39 oryza sativ
158	34	68.0	294	2	Q06104_YEAST	Q06104 saccharomyc	231	33	66.0	300	2	Q5M8S2_MOUSE	Q5M8S2 mus musculu
159	34	68.0	294	2	Q6B2S3_YEAST	Q6B2S3 saccharomyc	232	33	66.0	306	2	Q8WT15_PLACH	Q8WT15 plasmodium
160	34	68.0	321	2	Q61YV9_CAEBR	Q61YV9 caenorhabdi	233	33	66.0	306	2	Q8WT17_PLACH	Q8WT17 plasmodium
161	34	68.0	321	2	Q18648_CAEEL	Q18648 caenorhabdi	234	33	66.0	312	2	Q4FN80_9RICK	Q4FN80 candidatus
162	34	68.0	333	2	Q60872_CAEBR	Q60872 caenorhabdi	235	33	66.0	329	2	Q75LD6_ORYSA	Q75LD6 oryza sativ
163	34	68.0	369	2	Q6XCZ0_KLUOLA	Q6XCZ0 kluyveromyc	236	33	66.0	335	2	Q6MC54_PSAE	Q6MC54 pseudomonas
164	34	68.0	425	1	SYT4_MOUSE	P40749 mus musculu	237	33	66.0	335	2	Q9HW14_PSAE	Q9HW14 pseudomonas
165	34	68.0	425	1	SYT4_RAT	P50232 rattus norv	238	33	66.0	335	2	Q6MC54_PSAE	Q6MC54 pseudomonas
166	34	68.0	443	2	Q6MPA9_PAROW	Q6MPA9 parachlamyd	239	33	66.0	366	2	Q4YHU9_PLAVE	Q4YHU9 plasmodium
167	34	68.0	458	2	Q5XGK7_XENLA	Q5XGK7 xenopus lae	240	33	66.0	366	2	Q6CRJ8_KLUOLA	Q6CRJ8 kluyveromyc
168	34	68.0	486	2	Q6GZ13_TAXCU	Q6GZ13 taxus cuspi	241	33	66.0	373	2	Q75W95_BRARE	Q75W95 brachydanio
169	34	68.0	490	2	Q9LHP0_ARATH	Q9LHP0 arabisopsis	242	33	66.0	381	2	Q8H7G9_ARATH	Q8H7G9 arabisopsis
170	34	68.0	490	2	Q17840_CAEEL	Q17840 caenorhabdi	243	33	66.0	381	2	Q9FKA5_ARATH	Q9FKA5 arabisopsis
171	34	68.0	499	2	Q571C5_MOUSE	Q571C5 mus musculu	244	33	66.0	384	2	Q4N2V3_THPRA	Q4N2V3 theileria p
172	34	68.0	543	2	Q7Q9Y9_ANOGA	Q7Q9Y9 anopheles g	245	33	66.0	386	2	Q511V4_MAGGR	Q511V4 magnaporthe
173	34	68.0	550	2	Q59V64_CANAL	Q59V64 candida alb	246	33	66.0	390	2	Q5NRP0_SOLDE	Q5NRP0 solanum dem
174	34	68.0	575	2	Q4Z455_PLABE	Q4Z455 plasmodium	247	33	66.0	391	2	Q7Q5D8_ANOGA	Q7Q5D8 anopheles g
175	34	68.0	577	2	Q5NDB8_CHICK	Q5NDB8 gallus gall	248	33	66.0	399	2	Q4P315_USTWA	Q4P315 ustilago ma
176	34	68.0	583	2	Q55C09_DICDI	Q55C09 dictyosteli	249	33	66.0	399	2		
177	34	68.0	590	2	Q9LYK7_ARATH	Q9LYK7 arabisopsis	250	33	66.0				

32	36	72.0	537	1	Z029_XENLA	P18748 xenopus lae
33	36	72.0	543	2	Q4N480_THEPA	Q4n480 theileria p
34	36	72.0	552	2	Q4UFB2_THEAN	Q4ufb2 theileria a
35	36	72.0	557	2	Q5XWL7_SOLTU	Q5xwl7 solanum tub
36	36	72.0	742	2	Q9WAU7_9COMO	Q9wau7 broad bean
37	36	72.0	742	2	Q9WAU8_9COMO	Q9wau8 broad bean
38	36	72.0	742	2	Q9WAU9_9COMO	Q9wau9 broad bean
39	36	72.0	742	2	Q4WR8_9COMO	Q4wr8 broad bean
40	36	72.0	824	2	Q12663_9COMO	Q12663 broad bean
41	36	72.0	885	1	CYK3_YEAST	Q07533 saccharomyc
42	36	72.0	937	2	Q9WDH0_9COMO	Q9wdh0 broad bean
43	36	72.0	937	2	Q9Q202_9COMO	Q9q202 broad bean
44	36	72.0	1064	2	Q997C9_9COMO	Q997c9 broad bean
45	36	72.0	1064	2	Q9IR41_9COMO	Q9ir41 broad bean
46	36	72.0	1064	2	Q9IZU4_9COMO	Q9izu4 broad bean
47	36	72.0	1064	2	Q9YM09_9COMO	Q9ym09 broad bean
48	36	72.0	1064	2	Q9Z006_9COMO	Q9z006 patchouli m
49	36	72.0	1064	2	Q9WAU6_9COMO	Q9wau6 broad bean
50	36	72.0	1065	2	Q9Q2Q3_9COMO	Q9q2q3 broad bean
51	36	72.0	1482	2	Q8I3M8_PLAF7	Q8i3m8 plasmodium
52	36	72.0	2515	2	Q77365_PLAF7	Q77365 plasmodium
53	36	72.0	53	2	Q81B17_BACCR	Q81b17 bacillus ce
54	35	70.0	82	2	Q99MC1_RAT	Q99mc1 rattus norv
55	35	70.0	83	2	Q6GR61_XENLA	Q6gr61 xenopus lae
56	35	70.0	83	2	Q6P8B1_XENTR	Q6p8b1 xenopus tro
57	35	70.0	83	2	Q7T319_BRARE	Q7t319 brachydanio
58	35	70.0	102	2	Q80VH1_MOUSE	Q80vh1 mus musculu
59	35	70.0	117	2	Q4MIP5_BACCE	Q4mip5 bacillus ce
60	35	70.0	165	2	Q95QI9_CAEEL	Q95qi9 caenorhabdi
61	35	70.0	166	2	Q4MFY5_BACCE	Q4mfy5 bacillus ce
62	35	70.0	190	2	Q737L1_BACCI	Q737l1 bacillus ce
63	35	70.0	208	2	Q71T82_BPFI	Q71t82 bacterioph
64	35	70.0	231	2	Q4MNS6_BACCE	Q4mns6 bacillus ce
65	35	70.0	231	2	Q4MUV5_BACCE	Q4muvs6 bacillus ce
66	35	70.0	231	2	Q4MV30_BACCE	Q4mv30 bacillus ce
67	35	70.0	238	2	Q8N0E0_PLAVI	Q8n0e0 plasmodium
68	35	70.0	252	2	Q6XE32_9EUKA	Q6xe32 prymnesium
69	35	70.0	256	2	Q8N0D6_PLAVI	Q8n0d6 plasmodium
70	35	70.0	278	2	Q8MFT3_BACCE	Q8mft3 bacillus ce
71	35	70.0	287	2	Q9ULA6_HUMAN	Q9ula6 homo sapien
72	35	70.0	310	2	Q92X84_BPHLI	Q92xe4 bacterioph
73	35	70.0	329	2	Q9S6K4_BACTU	Q9s6k4 bacillus th
74	35	70.0	333	2	Q9CV75_MOUSE	Q9cv75 mus musculu
75	35	70.0	334	2	Q9Z5V3_BACTU	Q9z5v3 bacillus th
76	35	70.0	340	1	RPOA_ANTFO	Q85a01 anthoceros
77	35	70.0	344	2	Q13079_HUMAN	Q13079 homo sapien
78	35	70.0	374	2	Q8I7K5_CAEEL	Q8i7ks caenorhabdi
79	35	70.0	398	1	Y352_CLOBB	Q35838 clostridium
80	35	70.0	418	2	Q60P79_CABBR	Q60p79 caenorhabdi
81	35	70.0	462	1	NIFK_METMP	P71527 methanococc
82	35	70.0	475	2	Q5CIJ6_CRYHO	Q5cij6 cryptospori
83	35	70.0	477	1	T231F_BACTI	Q02404 bacillus th
84	35	70.0	477	2	Q4R514_WACFA	Q4r514 macaca fasc
85	35	70.0	477	2	Q5MR46_BACTU	Q5mra6 bacillus th
86	35	70.0	477	2	Q5MYT6_BACTI	Q5myt6 bacillus th
87	35	70.0	477	2	Q5U821_BACTT	Q5u821 bacillus th
88	35	70.0	477	2	Q7AL69_BACTU	Q7al69 bacillus th
89	35	70.0	477	2	Q8RLW1_BACTU	Q8rlw1 bacillus th
90	35	70.0	478	1	T231E_BACTF	Q02403 bacillus th
91	35	70.0	478	2	Q5MR47_BACTU	Q5mra7 bacillus th
92	35	70.0	478	2	Q5MR48_BACTF	Q5mra8 bacillus th
93	35	70.0	478	2	Q9X306_BACAN	Q9x306 bacillus an
94	35	70.0	478	2	Q4MI47_BACCE	Q4mi47 bacillus ce
95	35	70.0	478	2	Q4MJ44_BACCE	Q4mj44 bacillus ce
96	35	70.0	482	2	Q4MPJ7_BACCE	Q4mpj7 bacillus ce
97	35	70.0	486	2	Q4QGX4_LEIMA	Q4qgx4 leishmania
98	35	70.0	513	2	Q60VD6_CABBR	Q60vd6 caenorhabdi
99	35	70.0	529	2	Q61L87_CABBR	Q61l87 caenorhabdi
100	35	70.0	536	1	SNW1_HUMAN	Q13573 homo sapien
101	35	70.0	536	1	SNW1_MOUSE	Q9csn1 mus musculu
102	35	70.0	536	2	Q619E2_HUMAN	Q619e2 homo sapien
103	35	70.0	536	2	Q5R7R9_PONPY	Q5r7r9 pongo pygma
104	35	70.0	548	2	Q5CXI7_CRYPV	Q5cx17 cryptospori

OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 94.875 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-11
Perfect score: 50
Sequence: 1 PKKKFSGND 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	227	1	V45_VRSFL
2	45	80.0	204	1	V45_VRSFL
3	40	80.0	101	2	Q4MKK2_BACCE
4	40	80.0	354	2	Q4MIN9_BACCE
5	40	80.0	478	2	Q8KYQ6_BACILLUS AN
6	40	80.0	478	2	Q6EZW1_BACAN
7	39	78.0	191	1	RS7_BRAOL
8	39	78.0	347	2	Q4UFS1_THEAN
9	39	78.0	896	2	Q9FJ23_ARATH
10	38	76.0	89	2	Q21332_CAEEL
11	38	76.0	595	2	Q54HF5_DICDI
12	37	74.0	204	1	V45_VRSGE
13	37	74.0	204	1	V45_VRSMC
14	37	74.0	204	1	V45_VRSPE
15	37	74.0	373	2	Q71U48_LACCL
16	37	74.0	373	2	Q845A6_LACCL
17	37	74.0	571	2	Q7XE56_ORYSA
18	37	74.0	604	1	XJ13_YEAST
19	37	74.0	803	2	Q8IBJ5_PLAF7
20	37	74.0	1659	2	Q5AGQ3_CANAL
21	37	74.0	1661	2	Q5AGC3_CANAL
22	37	74.0	1664	1	INT1_CANAL
23	36	72.0	170	1	RUVK_AGRIS
24	36	72.0	170	1	RUVK_RHIME
25	36	72.0	223	2	Q98BA4_RHILLO
26	36	72.0	310	1	ODC1_YEAST
27	36	72.0	315	2	Q4IDZ5_GIBZE
28	36	72.0	478	1	T231C_BACTB
29	36	72.0	478	1	T231D_BACTB
30	36	72.0	478	2	Q5MRA5_BACTK
31	36	72.0	482	2	Q5DT40_BACTU

103	32	64.0	1428	2	C85079	hypothetical protei	176	30	60.0	265	2	H97324	uncharacterized pr
104	32	64.0	A48613	2	T22661	gag/pol polyprotei	177	30	60.0	265	2	S74282	hypothetical prote
105	32	64.0	1893	2	T22661	hypothetical prote	178	30	60.0	266	2	T06653	hypothetical prote
106	32	64.0	2437	2	S53611	MBP1 protein - ra	179	30	60.0	269	2	S73999	hypothetical prote
107	31.5	63.0	127	2	AP1253	hypothetical prote	180	30	60.0	269	2	T16487	hypothetical prote
108	31.5	63.0	1706	2	T39305	protein kinase - f	181	30	60.0	284	2	B69945	phase-related prot
109	31	62.0	91	2	T32495	hypothetical prote	182	30	60.0	285	2	G87298	short chain dehydr
110	31	62.0	99	2	S78739	protein YBL091C-a	183	30	60.0	302	2	E97323	probable epimerase
111	31	62.0	160	2	T87399	hypothetical prote	184	30	60.0	330	2	B65179	ribose operon repr
112	31	62.0	204	2	T15295	hypothetical prote	185	30	60.0	330	2	H86061	regulator for rbs
113	31	62.0	207	2	T07332	ribosomal protein	186	30	60.0	330	2	G91215	regulator for rbs
114	31	62.0	210	2	T14734	NS5 protein - sorg	187	30	60.0	330	2	G90256	DNA primase, proba
115	31	62.0	221	2	D91210	probable phosphata	188	30	60.0	332	2	AI0951	ribose operon repr
116	31	62.0	221	2	G86056	probable phosphata	189	30	60.0	355	2	AF1608	branched-chain fat
117	31	62.0	248	2	A39534	floral homeotic pr	190	30	60.0	358	2	JQ1292	hypothetical 39K p
118	31	62.0	257	2	AH1561	molybdate ABC tran	191	30	60.0	406	1	S18531	cytochrome P450 er
119	31	62.0	258	2	T39347	probable tricarbox	192	30	60.0	433	2	T19607	hypothetical prote
120	31	62.0	323	2	AC2481	hypothetical prote	193	30	60.0	440	2	B71293	hypothetical prote
121	31	62.0	325	2	B90023	conserved hypothet	194	30	60.0	448	2	S25324	hypothetical prote
122	31	62.0	330	2	T29640	mitochondrial carr	195	30	60.0	467	2	S41318	glutamate-ammonia
123	31	62.0	331	2	B95902	probable aldoketo	196	30	60.0	476	2	AB3575	hypothetical prote
124	31	62.0	331	2	A61046	edysone-induced m	197	30	60.0	492	2	T26502	hypothetical prote
125	31	62.0	392	2	A99592	hypothetical prote	198	30	60.0	496	2	T52112	deoxyribodipyrimid
126	31	62.0	393	2	A49008	paired box transcr	199	30	60.0	499	2	C85022	hypothetical prote
127	31	62.0	457	2	S03961	Ig mu chain C regi	200	30	60.0	513	2	T02002	hypothetical prote
128	31	62.0	469	2	B70201	hypothetical prote	201	30	60.0	514	2	T26501	hypothetical prote
129	31	62.0	478	2	A25122	transposase A - Ba	202	30	60.0	522	2	C96608	hypothetical prote
130	31	62.0	478	2	E29051	transposase B - Ba	203	30	60.0	526	2	F86618	glucose-6-p isomer
131	31	62.0	480	2	T00971	probable disease r	204	30	60.0	526	2	C72005	glucose-6-phosphat
132	31	62.0	501	2	G90534	prolyl-trna-synthe	205	30	60.0	539	2	B81533	phosphoenolpyruvat
133	31	62.0	554	1	NUVKL	glucose-6-phosphat	206	30	60.0	581	2	AG0017	hypothetical prote
134	31	62.0	557	1	T26638	hypothetical prote	207	30	60.0	581	2	T16915	hypothetical prote
135	31	62.0	571	2	T26638	beta-conglycinin a	208	30	60.0	598	2	T05329	CBP2 protein - yea
136	31	62.0	605	1	FWSXBA	beta-conglycinin a	209	30	60.0	630	1	BMBY	DNA gyrase B chain
137	31	62.0	605	1	S20007	probable serine/th	210	30	60.0	650	2	G97100	serine/threonine p
138	31	62.0	648	2	T04837	methy-accepting c	211	30	60.0	657	2	C97113	hypothetical prote
139	31	62.0	652	2	G82401	auxin response fac	212	30	60.0	662	2	T20570	multifunctional am
140	31	62.0	665	2	D96621	serine/threonine p	213	30	60.0	688	2	S46774	hypothetical prote
141	31	62.0	728	2	T43632	gene bobby sox pro	214	30	60.0	736	2	T25447	phospholipase C (E
142	31	62.0	769	2	T08431	serine/threonine p	215	30	60.0	751	2	JC8057	disease resistance
143	31	62.0	792	2	T43630	hypothetical prote	216	30	60.0	776	2	S45495	lep4 protein - fis
144	31	62.0	795	2	D64343	hypothetical prote	217	30	60.0	789	2	T28714	hypothetical prote
145	31	62.0	798	2	T33673	hypothetical prote	218	30	60.0	796	2	AG0523	glucose dehydrogen
146	31	62.0	881	2	T28013	hypothetical prote	219	30	60.0	803	2	B82099	surface antigen VC
147	31	62.0	903	2	C82516	hypothetical prote	220	30	60.0	831	2	S39835	hypothetical prote
148	31	62.0	919	2	S45298	retinoblastoma-ass	221	30	60.0	831	2	A32262	fatty-acid synthas
149	31	62.0	945	2	S48369	26S proteasome reg	222	30	60.0	838	2	A32262	hypothetical prote
150	31	62.0	1007	2	T42219	alpha-mannosidase	223	30	60.0	846	2	F83388	S-receptor kinase
151	31	62.0	1075	2	T27623	hypothetical prote	224	30	60.0	854	2	T14377	99.9K hypothetical
152	31	62.0	1080	2	T27622	hypothetical prote	225	30	60.0	907	2	A86460	isooleucyl-tRNA syn
153	31	62.0	1229	2	F90040	respiratory nitrat	226	30	60.0	967	2	AH2660	isooleucyl-tRNA syn
154	31	62.0	1254	2	T30855	multidrug resistat	227	30	60.0	967	2	F97442	gene 23 protein -
155	31	62.0	1835	2	S46082	urea carboxylase (228	30	60.0	1020	1	WZ8EB5	segment protein 2
156	30.5	61.0	509	2	T37593	hypothetical prote	229	30	60.0	1021	2	T42566	cellulose synthase
157	30.5	61.0	732	2	S46352	env polyprotein -	230	30	60.0	1026	2	T51579	H+-exporting ATPas
158	30	60.0	79	2	A82667	single-stranded DN	231	30	60.0	1131	2	S34213	protein F40512.2 (
159	30	60.0	118	2	D82777	type 4 fibriar as	232	30	60.0	1245	2	G88104	hypothetical prote
160	30	60.0	148	2	C82799	single-stranded DN	233	30	60.0	1245	2	T31953	hypothetical prote
161	30	60.0	151	2	H82654	single-stranded DN	234	30	60.0	1276	2	S11455	botulinum neurotox
162	30	60.0	184	2	T43321	ribosomal protein	235	30	60.0	1285	2	S70582	botulinum neurotox
163	30	60.0	189	2	T22034	hypothetical prote	236	30	60.0	1291	2	A97777	botulinum neurotox
164	30	60.0	189	2	T43516	ribosomal protein	237	30	60.0	1355	2	S46431	hypothetical prote
165	30	60.0	189	2	C81428	peptidyl-prolyl ci	238	30	60.0	1355	2	T28715	hypothetical prote
166	30	60.0	191	2	S62409	40S ribosomal prot	239	30	60.0	1440	1	SYHUQT	probable transcrip
167	30	60.0	191	2	B84740	hypothetical prote	240	30	60.0	1588	2	T38660	multifunctional am
168	30	60.0	192	2	T40083	40S ribosomal prot	241	30	60.0	1714	1	S18644	multifunctional am
169	30	60.0	195	2	S31287	ribosomal protein	242	30	60.0	1785	2	T21558	hypothetical prote
170	30	60.0	197	1	S16832	ribosomal protein	243	30	60.0	1929	2	T21559	hypothetical prote
171	30	60.0	202	2	A64480	hypothetical prote	244	30	60.0	2505	1	XYRTFA	enoyl-(acyl)-carrie
172	30	60.0	218	2	T31642	hypothetical prote	245	30	60.0	2509	2	G01880	fatty-acid synthas
173	30	60.0	218	2	T01104	hypothetical prote	246	30	60.0	2514	2	F81045	hemagglutinin/hemo
174	30	60.0	231	2	B84965	disease resistance	247	30	60.0	2514	2	F81045	peptidyl-prolyl ci
175	30	60.0	233	2	AD2041	phosphoglycerate m	248	29	58.0	110	2	S82781	hypothetical prote
						hypothetical prote							

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 15 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-11

Perfect score: 50

Sequence: 1 PKKKFSGND 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	50.0	204	A44583	venom allergen ant
2	38	76.0	89	T23462	hypothetical prote
3	37	74.0	204	B37329	antigen 5 - easter
4	37	74.0	204	B44583	venom allergen ant
5	37	74.0	204	C44583	venom allergen ant
6	37	74.0	604	S56027	hypothetical prote
7	37	74.0	1664	T18216	integrin-like prot
8	36	72.0	170	AH3014	Holliday Junction
9	36	72.0	310	S69050	hypothetical prote
10	36	72.0	310	S69050	probable membrane
11	36	72.0	399	E33282	DNA-binding protei
12	36	72.0	478	S25199	transposase - Bac
13	36	72.0	478	C29051	transposase C - Ba
14	36	72.0	885	S67660	hypothetical prote
15	36	72.0	2523	T18477	hypothetical prote
16	35	70.0	310	T13528	hypothetical prote
17	35	70.0	344	G01628	protein containing
18	35	70.0	398	H96967	nitrogenase (EC 1.
19	35	70.0	462	T10094	transposase - Bac
20	35	70.0	477	S25822	hypothetical prote
21	35	70.0	478	C59095	transposase - Bac
22	35	70.0	478	S25821	hypothetical prote
23	35	70.0	561	T16148	hypothetical prote
24	35	70.0	1007	T24643	DNA-directed DNA p
25	35	70.0	1017	T30195	hypothetical prote
26	35	70.0	1480	T05566	major blood-stage
27	35	70.0	1751	A45604	hypothetical prote
28	35	70.0	2504	A57788	enoyl-(acyl-carrie
29	34	68.0	294	S59774	probable membrane

30	34	68.0	321	2	T24410	hypothetical prote
31	34	68.0	425	2	I59355	synaptotagmin IV -
32	34	68.0	490	2	T21365	hypothetical prote
33	34	68.0	590	2	T48625	pescadillo-like pr
34	34	68.0	1619	2	T30541	ABC1 transport pro
35	33	66.0	87	2	T03993	hypothetical prote
36	33	66.0	111	1	CCRG2	cytochrome c2 - Ag
37	33	66.0	139	2	C99192	cytochrome c2 [imp
38	33	66.0	139	2	AG3094	40S ribosomal prot
39	33	66.0	190	2	T51483	hypothetical prote
40	33	66.0	190	2	B3689	probable 40S ribos
41	33	66.0	191	2	A96526	hypothetical prote
42	33	66.0	335	2	G83088	hypothetical prote
43	33	66.0	437	2	S46796	hypothetical prote
44	33	66.0	458	2	S52594	chromosome segrega
45	33	66.0	673	2	T41768	ACKNPV orf23 - Bom
46	33	66.0	690	2	G72852	copia-like envelop
47	33	66.0	700	2	S09699	bib protein - frui
48	33	66.0	713	2	S84437	probable membrane
49	33	66.0	728	2	F84500	hypothetical prote
50	33	66.0	1159	2	S62562	probable nuclear p
51	33	66.0	1334	2	B86451	probable copia-typ
52	33	66.0	1356	2	P84486	probable retroelem
53	33	66.0	1432	2	B85431	trichohyalin like
54	33	66.0	1726	2	A39401	merozoite surface
55	33	66.0	1840	1	CHRTM1	sodium channel pro
56	33	66.0	1879	2	T19481	hypothetical prote
57	33	66.0	1951	2	S00320	sodium channel pro
58	33	66.0	1976	2	I56555	sodium channel pro
59	33	66.0	1983	2	A60054	sodium channel alp
60	33	66.0	2005	2	A46269	sodium channel alp
61	33	66.0	2005	2	B25019	sodium channel pro
62	33	66.0	2009	2	A25019	sodium channel pro
63	33	66.0	2302	2	T14328	protein-tyrosine-p
64	32	64.0	88	2	A40485	nucleocapsid prote
65	32	64.0	161	2	C54270	insulin-like growt
66	32	64.0	186	2	DB1360	cytochrome C Cj087
67	32	64.0	264	2	JC4111	triacylglycerol li
68	32	64.0	276	2	T49220	casein kinase II (
69	32	64.0	308	2	T26716	hypothetical prote
70	32	64.0	308	2	T30152	hypothetical prote
71	32	64.0	345	2	T06098	hypothetical prote
72	32	64.0	351	2	A81132	sulfate ABC transp
73	32	64.0	366	2	T47360	hypothetical prote
74	32	64.0	378	2	T06512	DNA-binding protei
75	32	64.0	384	2	S76163	hypothetical prote
76	32	64.0	403	2	C70385	hypothetical prote
77	32	64.0	417	2	S76588	hypothetical prote
78	32	64.0	465	2	A55518	hypothetical prote
79	32	64.0	524	2	B1678	glucose-6-phosphat
80	32	64.0	524	2	E96494	protein F7F22.8 [i
81	32	64.0	548	2	A81854	glucose-6-phosphat
82	32	64.0	548	2	C81089	glucose-6-phosphat
83	32	64.0	614	2	T16268	hypothetical prote
84	32	64.0	653	2	F75005	aldehyde-ferredoxi
85	32	64.0	653	2	B71157	hypothetical prote
86	32	64.0	675	2	F85071	hypothetical prote
87	32	64.0	701	1	FOFVIR	gag polyprotein -
88	32	64.0	701	2	S11454	gag polyprotein -
89	32	64.0	701	2	F48613	gag polyprotein -
90	32	64.0	701	2	F48613	gag polyprotein -
91	32	64.0	701	2	S35430	gag polyprotein -
92	32	64.0	740	2	T09480	hypothetical prote
93	32	64.0	758	2	T39628	hypothetical prote
94	32	64.0	774	2	T22309	hypothetical prote
95	32	64.0	787	2	PC1232	copia polyprotein
96	32	64.0	802	2	C83588	probable hydroxama
97	32	64.0	866	2	B85075	probable athlia tr
98	32	64.0	871	2	T45692	receptor-like prot
99	32	64.0	889	2	T47311	hypothetical prote
100	32	64.0	1079	1	T9FVMI	gag-Rml1-env polyP
101	32	64.0	1409	1	OFFFCP	copia polyprotein
102	32	64.0	1409	1	OFFFCP	copia polyprotein

98	33	66.0	191	3	AAG08429	Aag08429 Arabidops	171	33	66.0	1951	9	AEA44252	Aea44252 Rat sodiu
99	33	66.0	191	3	AAG34639	Aag34639 Arabidops	172	33	66.0	1951	9	AEA44250	Aea44250 Human SCN
100	33	66.0	191	3	AAG19869	Aag19869 Arabidops	173	33	66.0	1959	6	AAE37322	Aae37322 Human ion
101	33	66.0	192	3	AAG40892	Aag40892 Zea mays	174	33	66.0	1962	5	AAE20511	Aae20511 Human ion
102	33	66.0	192	6	ABP96240	Abp96240 Human nuc	175	33	66.0	1973	5	AAE20516	Aae20516 Human ion
103	33	66.0	194	8	ADY05236	Ady05236 Plant ful	176	33	66.0	1976	7	ADSE57386	Adse57386 Rat Prote
104	33	66.0	194	8	ADX75553	Adx75553 Plant ful	177	33	66.0	1978	2	AAW69361	Aaw69361 Tetradoto
105	33	66.0	195	8	ADX88416	Adx88416 Plant ful	178	33	66.0	1978	9	ADX26338	Adx26338 Novel cel
106	33	66.0	205	8	ADX72834	Adx72834 Plant ful	179	33	66.0	1979	3	AEA44245	Aea44245 Murine so
107	33	66.0	209	8	ADX96710	Adx96710 Plant ful	180	33	66.0	1980	3	AAE23563	Aae23563 Human sod
108	33	66.0	212	8	ADY07237	Ady07237 Plant ful	181	33	66.0	1980	5	AAO14927	Aao14927 Human sod
109	33	66.0	213	8	ADY04691	Ady04691 Plant ful	182	33	66.0	1980	7	ADB78600	Adb78600 Human sod
110	33	66.0	213	8	ADX78346	Adx78346 Plant ful	183	33	66.0	1980	7	ADB78605	Adb78605 Human sod
111	33	66.0	215	8	ADX97096	Adx97096 Plant ful	184	33	66.0	1980	7	ADZ88372	Adz88372 Human SCN
112	33	66.0	216	8	ADX96791	Adx96791 Plant ful	185	33	66.0	1981	7	ADZ88372	Adz88372 Human SCN
113	33	66.0	217	5	ABG60158	Abg60158 Human DIT	186	33	66.0	1988	2	AAW69362	Aaw69362 Tetradoto
114	33	66.0	217	6	ABU11632	Abu11632 Human MDD	187	33	66.0	1988	2	AAW69362	Aaw69362 Tetradoto
115	33	66.0	217	6	ADX96954	Adx96954 Plant ful	188	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
116	33	66.0	217	8	ADX78915	Adx78915 Plant ful	189	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
117	33	66.0	217	8	ADX96694	Adx96694 Plant ful	190	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
118	33	66.0	217	8	ADX96978	Adx96978 Plant ful	191	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
119	33	66.0	217	8	ADY04643	Ady04643 Plant ful	192	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
120	33	66.0	222	8	ADX75722	Adx75722 Plant ful	193	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
121	33	66.0	223	4	ABU72887	Abu72887 Human/mou	194	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
122	33	66.0	233	6	ABU62255	Abu62255 Human/mou	195	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
123	33	66.0	233	7	ADC17399	Adc17399 Human/mou	196	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
124	33	66.0	309	3	ABO3656	Abob3656 Clone 5 v	197	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
125	33	66.0	309	3	ABO3655	Abob3655 Clone 3 v	198	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
126	33	66.0	309	3	ABO3657	Abob3657 Clone 6 v	199	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
127	33	66.0	312	7	ADC96303	Adc96303 E. faeciu	200	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
128	33	66.0	314	6	ABU72885	Abu72885 Murine zt	201	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
129	33	66.0	314	6	ABU62253	Abu62253 Mouse try	202	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
130	33	66.0	314	7	ADC17377	Adc17377 Mouse ser	203	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
131	33	66.0	336	7	ABO75389	Abob75389 Pseudomon	204	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
132	33	66.0	366	8	ADY08192	Ady08192 Plant ful	205	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
133	33	66.0	368	3	AAG26449	Aag26449 Arabidops	206	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
134	33	66.0	369	3	AAG47270	Aag47270 Arabidops	207	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
135	33	66.0	381	3	AAG47292	Aag47292 Arabidops	208	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
136	33	66.0	381	3	AAG26698	Aag26698 Arabidops	209	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
137	33	66.0	458	6	ABR53834	Abbr53834 Protein s	210	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
138	33	66.0	458	6	ABU44976	Abu44976 Disease t	211	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
139	33	66.0	540	6	ABU24461	Abu24461 Protein e	212	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
140	33	66.0	570	4	ABG20671	Abg20671 Novel hum	213	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
141	33	66.0	614	8	ADY05411	Ady05411 Plant ful	214	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
142	33	66.0	619	8	ADY05478	Ady05478 Plant ful	215	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
143	33	66.0	621	8	ADY07025	Ady07025 Plant ful	216	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
144	33	66.0	655	5	ABG97460	Abg97460 S. kaniha	217	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
145	33	66.0	655	9	ABE12693	Abe12693 Emedlyne	218	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
146	33	66.0	655	9	ABE12693	Abe12693 Streptomy	219	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
147	33	66.0	696	4	ABB60920	Abb60920 Drosophil	220	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
148	33	66.0	702	8	ADG27023	Adg27023 Human OAT	221	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
149	33	66.0	702	8	ADM79590	Adm79590 Human liv	222	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
150	33	66.0	702	8	ADQ88228	Adq88228 Human 536	223	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
151	33	66.0	713	6	ABR53234	Abrr53234 Protein s	224	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
152	33	66.0	713	7	ADK63692	Adk63692 Disease t	225	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
153	33	66.0	805	4	AAU47293	Aau47293 Propionib	226	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
154	33	66.0	805	6	ABM43812	Abm43812 Propionib	227	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
155	33	66.0	851	8	ADH41623	Adh41623 Novel hum	228	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
156	33	66.0	855	5	AAO18737	Aao18737 Human NOV	229	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
157	33	66.0	943	5	ABE93634	Abbe93634 Herbicida	230	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
158	33	66.0	943	5	ABE27326	Abbe27326 Pinus rad	231	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
159	33	66.0	1510	9	ADZ88370	Adz88370 Mutant SC	232	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
160	33	66.0	1726	9	ADZ88370	Adz88370 Human SCN	233	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
161	33	66.0	1795	7	ADB78596	Adb78596 Human sod	234	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
162	33	66.0	1855	7	ADB78597	Adb78597 Human sod	235	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
163	33	66.0	1891	9	ADY27145	Ady27145 Human SCN	236	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
164	33	66.0	1942	8	ADZ87534	Adz87534 Mutant SC	237	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
165	33	66.0	1950	7	ADB78607	Adb78607 Human sod	238	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
166	33	66.0	1951	4	ABR99678	Aabr99678 Human adu	239	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
167	33	66.0	1951	4	ABR99678	Aabr99678 Human neo	240	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
168	33	66.0	1951	7	ADSE5628	Adse5628 Rat Prote	241	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
169	33	66.0	1951	8	ADL06576	Adl06576 Human tum	242	33	66.0	1988	7	ABR83184	Abr83184 Human SCN
170	33	66.0	1951	8	ADP79543	Adp79543 Human sod	243	33	66.0	1988	7	ABR83184	Abr83184 Human SCN

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 79.125 Seconds
(without alignments)
49.977 Million cell updates/sec

Title: US-10-091-135-11

Perfect score: 50

Sequence: 1 PKKFGSND 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1908s.*
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- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	AAE28817	Aae28817 Vespula v
2	50	100.0	25	AAW35671	Aaw35671 T cell pe
3	50	100.0	48	AAE28813	Aae28813 Vespula v
4	50	100.0	204	AAW35688	Aaw35688 Vespulid an
5	50	100.0	204	AAV45217	Aav45217 Wild type
6	50	100.0	204	ABG66977	Abg66977 Wasp veno
7	50	100.0	204	ABG67052	Abg67052 Wasp veno
8	50	100.0	204	ABG67104	Abg67104 Wasp veno
9	50	100.0	204	ABG67103	Abg67103 Wasp veno
10	50	100.0	204	AAE28820	Aae28820 Vespula v
11	50	100.0	209	ABM00031	Abm00031 Allergen
12	50	100.0	227	AAV25644	Aav25644 Vespula s
13	50	100.0	227	AAE13071	Aae13071 Vespula v
14	50	100.0	227	ADC34893	Adc34893 Wasp alle
15	44	88.0	204	ABG66983	Abg66983 Wasp veno
16	37	74.0	25	AAW35670	Aaw35670 T cell pe
17	37	74.0	62	ABG60195	Abg60195 Human DIT
18	37	74.0	62	ABR41712	AbR41712 Human DIT
19	37	74.0	204	AAW35687	Aaw35687 Vespulid an
20	37	74.0	1664	AAW99462	Aaw99462 C.albican
21	37	74.0	1664	AAE19799	Aae19799 Candida a
22	37	74.0	1664	AAU79331	Aau79331 Candida a
23	37	74.0	1664	ADC73265	Adc73265 Yeast Int
24	37	74.0	1664	ADM33264	Adm33264 Candida a

25	36	72.0	223	5	ABP08441	Abp08441 Human ORP
26	36	72.0	310	5	ADS64665	Ads64665 Saccharom
27	36	72.0	310	8	ADS44042	Ads44042 Bacterial
28	36	72.0	885	7	ADBG2184	Adbg2184 Disease t
29	35	70.0	34	7	ADB67822	Adb67822 Human lun
30	35	70.0	52	4	AAAI14630	Aaai14630 Peptide #
31	35	70.0	52	4	AAAB33590	Aaab33590 Peptide #
32	35	70.0	52	4	AAAM27051	Aaam27051 Peptide #
33	35	70.0	52	4	ABBA28410	Abba28410 Peptide #
34	35	70.0	52	4	ABBI19047	Abbi19047 Protein #
35	35	70.0	52	4	AAAM66764	Aaam66764 Human bon
36	35	70.0	52	4	AAAM54365	Aaam54365 Human bra
37	35	70.0	52	4	ABG48433	Abg48433 Human liv
38	35	70.0	52	4	AAAM02355	Aaam02355 Peptide #
39	35	70.0	52	5	ABG36419	Abg36419 Human pep
40	35	70.0	146	4	ABGI15537	Abgi15537 Novel hum
41	35	70.0	183	4	ABGI10599	Abgi10599 Novel hum
42	35	70.0	500	7	ADC37415	Adc37415 Nuclear f
43	35	70.0	536	7	ADC37417	Adc37417 Nuclear f
44	35	70.0	536	7	ADC37419	Adc37419 Nuclear f
45	35	70.0	536	8	ADU60296	Adu60296 Housekeep
46	35	70.0	613	4	ABG22924	Abg22924 Novel hum
47	35	70.0	666	2	AAW13729	Aaw13729 Herbicide
48	35	70.0	858	5	ABB93619	Abb93619 Herbicide
49	35	70.0	942	4	ABGI0600	Abgi0600 Novel hum
50	35	70.0	1134	4	AAU28072	Aau28072 Novel hum
51	35	70.0	1134	9	ADX05983	Adx05983 Cyclin-de
52	35	70.0	1398	5	ABG97491	Abg97491 Human NOV
53	35	70.0	1400	4	ABR83348	Abr83348 AAP-2 pro
54	35	70.0	1445	6	ABR41365	Abr41365 Human DIT
55	35	70.0	2504	5	ABP54923	Abp54923 Human fat
56	34	68.0	72	5	ABP38211	Abp38211 Staphyloc
57	34	68.0	78	4	AAO11095	Aao11095 Human pol
58	34	68.0	290	8	ADX76571	Adx76571 Plant ful
59	34	68.0	384	4	AAAB62726	Aaab62726 Borrelia
60	34	68.0	408	4	AAAB62737	Aaab62737 Borrelia
61	34	68.0	425	7	ADDE62214	Adde62214 Rat Prote
62	34	68.0	425	7	ADDE62214	Adde62214 Rat Prote
63	34	68.0	425	7	ADDE62206	Adde62206 Rat Prote
64	34	68.0	425	7	ADDE62202	Adde62202 Rat Prote
65	34	68.0	425	7	ADDE62210	Adde62210 Rat Prote
66	34	68.0	550	5	ABP73370	Abp73370 Candida a
67	34	68.0	654	4	ABBB63266	Abbb63266 Drosophil
68	34	68.0	688	4	ABBB63269	Abbb63269 Drosophil
69	34	68.0	775	9	AEA04751	Aea04751 CCH-type
70	34	68.0	793	7	ADC96596	Adc96596 E. faeciu
71	34	68.0	882	6	ADA33945	Ada33945 Acinetoba
72	34	68.0	882	6	ADA33945	Ada33945 Acinetoba
73	34	68.0	974	7	ABO74894	AbO74894 Pseudomon
74	34	68.0	1032	8	ADR86313	Adr86313 Aspergill
75	33	66.0	10	4	AAAG87510	Aag87510 Saccharom
76	33	66.0	24	2	AAAR78976	Aar78976 Peptide i
77	33	66.0	45	3	AAAG58445	Aag58445 Arabidops
78	33	66.0	59	3	AAAG15655	Aag15655 Arabidops
79	33	66.0	86	3	AAAG59326	Aag59326 Arabidops
80	33	66.0	86	3	AAAG06947	Aag06947 Arabidops
81	33	66.0	86	3	AAAG58444	Aag58444 Arabidops
82	33	66.0	86	4	AAAO03946	Aao03946 Human pol
83	33	66.0	87	3	AAAG58443	Aag58443 Arabidops
84	33	66.0	87	3	AAAG59325	Aag59325 Arabidops
85	33	66.0	87	3	AAAG06946	Aag06946 Arabidops
86	33	66.0	101	4	AAAO1614	Aao01614 Human pol
87	33	66.0	110	3	AAAG15654	Aag15654 Arabidops
88	33	66.0	124	3	AAAG41041	Aag41041 Zea mays
89	33	66.0	139	3	AAAB24692	Aab24692 Plant SDF
90	33	66.0	140	3	AAAB24669	Aab24669 Plant SDF
91	33	66.0	141	3	AAAG60995	Aag60995 Arabidops
92	33	66.0	154	3	AAAG41040	Aag41040 Zea mays
93	33	66.0	170	3	AAAG44967	Aag44967 Zea mays
94	33	66.0	182	3	AAAG60994	Aag60994 Arabidops
95	33	66.0	183	3	AAAG60993	Aag60993 Arabidops
96	33	66.0	190	3	AAAB24691	Aab24691 Plant SDF
97	33	66.0	191	3	AAAB24668	Aab24668 Plant SDF

99	30	53.6	920	7	US-11-087-099-11404	Sequence 11404, A	172	29	51.8	382	7	US-11-096-568A-16256	Sequence 16256, A
100	30	53.6	920	7	US-11-188-298-21540	Sequence 21540, A	173	29	51.8	384	7	US-11-188-298-8581	Sequence 8581, Ap
101	30	53.6	1027	7	US-11-024-959-324	Sequence 324, App	174	29	51.8	384	7	US-11-188-298-14898	Sequence 14898, A
102	30	53.6	1062	7	US-11-188-298-7429	Sequence 7429, Ap	175	29	51.8	407	7	US-11-018-868-43	Sequence 43, Appl
103	30	53.6	1305	7	US-11-188-298-19455	Sequence 19455, A	176	29	51.8	417	7	US-11-096-568A-30282	Sequence 30282, A
104	30	53.6	1416	7	US-11-128-059-60	Sequence 60, Appl	177	29	51.8	417	7	US-11-096-568A-33043	Sequence 33043, A
105	30	53.6	1494	7	US-11-128-059-78	Sequence 78, Appl	178	29	51.8	424	7	US-11-096-568A-30281	Sequence 30281, A
106	30	53.6	1706	7	US-11-052-554A-176	Sequence 176, App	179	29	51.8	424	7	US-11-096-568A-33042	Sequence 33042, A
107	30	53.6	2086	7	US-11-128-059-82	Sequence 82, Appl	180	29	51.8	431	7	US-11-079-463-5692	Sequence 5692, Ap
108	30	53.6	2313	7	US-11-128-059-80	Sequence 80, Appl	181	29	51.8	462	7	US-11-188-298-566	Sequence 566, App
109	30	53.6	2358	7	US-11-128-059-74	Sequence 74, Appl	182	29	51.8	465	6	US-10-467-657-1292	Sequence 1292, Ap
110	30	53.6	2439	7	US-11-128-059-76	Sequence 76, Appl	183	29	51.8	465	7	US-11-087-099-3381	Sequence 3381, Ap
111	30	53.6	2458	7	US-11-128-059-94	Sequence 94, Appl	184	29	51.8	471	7	US-11-087-099-3188	Sequence 3188, Ap
112	30	53.6	2551	6	US-10-453-372-256	Sequence 256, App	185	29	51.8	471	7	US-11-188-298-14044	Sequence 14044, A
113	30	53.6	2551	7	US-11-128-059-96	Sequence 96, Appl	186	29	51.8	479	7	US-11-074-176-168	Sequence 168, App
114	30	53.6	7465	7	US-11-087-099-7521	Sequence 7521, Ap	187	29	51.8	480	6	US-10-821-234-886	Sequence 886, App
115	29	51.8	95	6	US-10-997-081A-25	Sequence 25, Appl	188	29	51.8	504	7	US-11-155-492-73	Sequence 73, Appl
116	29	51.8	97	6	US-10-997-081A-11	Sequence 11, Appl	189	29	51.8	561	7	US-11-096-568A-33041	Sequence 33041, A
117	29	51.8	97	6	US-10-997-081A-18	Sequence 18, Appl	190	29	51.8	614	7	US-11-155-492-107	Sequence 107, App
118	29	51.8	97	6	US-10-997-081A-19	Sequence 19, Appl	191	29	51.8	616	7	US-11-155-492-3	Sequence 3, Appl
119	29	51.8	97	6	US-10-997-081A-20	Sequence 20, Appl	192	29	51.8	627	6	US-11-188-298-8089	Sequence 8089, Ap
120	29	51.8	97	6	US-10-997-081A-21	Sequence 21, Appl	193	29	51.8	629	6	US-10-506-454-236	Sequence 236, App
121	29	51.8	97	6	US-10-997-081A-22	Sequence 22, Appl	194	29	51.8	635	6	US-10-523-503-38	Sequence 38, Appl
122	29	51.8	97	6	US-10-997-081A-23	Sequence 23, Appl	195	29	51.8	635	7	US-11-188-298-13361	Sequence 13361, A
123	29	51.8	97	6	US-10-997-081A-40	Sequence 40, Appl	196	29	51.8	660	7	US-11-188-298-135	Sequence 135, App
124	29	51.8	97	6	US-10-997-081A-41	Sequence 41, Appl	197	29	51.8	708	6	US-10-821-234-917	Sequence 917, App
125	29	51.8	113	7	US-11-096-568A-5527	Sequence 5527, Ap	198	29	51.8	745	7	US-11-079-463-8524	Sequence 8524, Ap
126	29	51.8	114	7	US-11-096-568A-21191	Sequence 21191, A	199	29	51.8	791	6	US-10-467-657-5014	Sequence 5014, Ap
127	29	51.8	140	7	US-11-096-568A-21190	Sequence 21190, A	200	29	51.8	874	6	US-10-510-386-28	Sequence 28, Appl
128	29	51.8	149	7	US-11-096-568A-21189	Sequence 21189, A	201	29	51.8	1047	6	US-10-510-386-200	Sequence 200, App
129	29	51.8	153	7	US-11-087-099-6556	Sequence 6556, Ap	202	29	51.8	1329	7	US-11-052-554A-136	Sequence 136, App
130	29	51.8	184	7	US-11-096-568A-33564	Sequence 33564, A	203	29	51.8	1329	7	US-11-087-099-882	Sequence 882, App
131	29	51.8	214	7	US-11-096-568A-5526	Sequence 5526, Ap	204	29	51.8	1366	6	US-10-821-234-1431	Sequence 1431, Ap
132	29	51.8	227	6	US-10-982-357-75	Sequence 75, App	205	29	51.8	1366	7	US-11-186-284-31	Sequence 31, Appl
133	29	51.8	227	6	US-10-982-357-76	Sequence 76, App	206	29	51.8	1408	7	US-11-087-099-8482	Sequence 8482, Ap
134	29	51.8	227	6	US-10-982-357-75	Sequence 75, App	207	29	51.8	1408	7	US-11-087-099-8482	Sequence 8482, Ap
135	29	51.8	236	6	US-10-506-454-783	Sequence 783, App	208	29	51.8	1408	7	US-11-087-099-8482	Sequence 8482, Ap
136	29	51.8	249	7	US-11-096-568A-12681	Sequence 12681, A	209	28.5	50.9	1408	7	US-11-087-099-8482	Sequence 8482, Ap
137	29	51.8	249	7	US-11-096-568A-14903	Sequence 14903, A	210	28.5	50.9	1408	7	US-11-087-099-8482	Sequence 8482, Ap
138	29	51.8	268	7	US-11-096-568A-7693	Sequence 7693, Ap	211	28.5	50.9	1408	7	US-11-087-099-8482	Sequence 8482, Ap
139	29	51.8	289	7	US-11-087-099-5569	Sequence 5569, Ap	212	28.5	50.9	1408	7	US-11-087-099-8482	Sequence 8482, Ap
140	29	51.8	290	7	US-11-096-568A-33563	Sequence 33563, A	213	28.5	50.9	1408	7	US-11-087-099-8482	Sequence 8482, Ap
141	29	51.8	294	7	US-11-087-099-2961	Sequence 2961, Ap	214	28.5	50.9	1408	7	US-11-087-099-8482	Sequence 8482, Ap
142	29	51.8	300	7	US-11-151-601-17	Sequence 17, Appl	215	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
143	29	51.8	300	7	US-11-188-298-4053	Sequence 4053, Ap	216	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
144	29	51.8	301	7	US-11-188-298-10923	Sequence 10923, A	217	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
145	29	51.8	301	7	US-11-188-298-16822	Sequence 16822, A	218	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
146	29	51.8	302	7	US-11-096-568A-27830	Sequence 27830, A	219	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
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148	29	51.8	308	7	US-11-096-568A-14902	Sequence 14902, A	221	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
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152	29	51.8	313	7	US-11-079-463-8903	Sequence 8903, Ap	225	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
153	29	51.8	315	7	US-11-188-298-12085	Sequence 12085, A	226	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
154	29	51.8	317	7	US-11-096-568A-33562	Sequence 33562, A	227	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
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156	29	51.8	322	7	US-11-079-463-7056	Sequence 7056, Ap	229	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
157	29	51.8	334	7	US-11-096-568A-12679	Sequence 12679, A	230	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
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159	29	51.8	350	7	US-11-082-389-90	Sequence 90, Appl	232	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
160	29	51.8	360	7	US-11-082-389-92	Sequence 92, Appl	233	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
161	29	51.8	362	7	US-11-188-298-9074	Sequence 9074, Ap	234	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
162	29	51.8	368	6	US-10-194-487-338	Sequence 338, App	235	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
163	29	51.8	368	6	US-10-195-883-338	Sequence 338, App	236	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
164	29	51.8	368	6	US-10-195-888-338	Sequence 338, App	237	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
165	29	51.8	368	6	US-10-195-889-338	Sequence 338, App	238	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
166	29	51.8	369	7	US-11-096-568A-7691	Sequence 7691, Ap	239	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
167	29	51.8	370	7	US-11-096-568A-16257	Sequence 16257, A	240	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap
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171	29	51.8	377	6	US-10-517-939-142	Sequence 142, App	244	28	50.0	1408	7	US-11-087-099-8482	Sequence 8482, Ap

101	33	58.9	184	4	US-10-425-115-248707	Sequence 248707,	174	32	57.1	202	5	US-10-450-763-54536	Sequence 54536, A
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105	33	58.9	251	4	US-10-767-701-34953	Sequence 34953, A	178	32	57.1	234	5	US-10-732-923-16095	Sequence 16095, A
106	33	58.9	270	4	US-10-425-114-71386	Sequence 71386, A	179	32	57.1	235	4	US-10-282-122A-52331	Sequence 52331, A
107	33	58.9	284	4	US-10-425-115-274099	Sequence 274099, A	180	32	57.1	238	4	US-10-424-599-24472	Sequence 24472, A
108	33	58.9	331	4	US-10-425-114-60525	Sequence 60525, A	181	32	57.1	271	4	US-10-389-566-923	Sequence 923, App
109	33	58.9	346	4	US-10-369-493-7890	Sequence 7890, Ap	182	32	57.1	281	5	US-10-732-923-16629	Sequence 16629, A
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112	33	58.9	390	4	US-10-282-122A-57225	Sequence 57225, A	185	32	57.1	292	4	US-10-424-599-272756	Sequence 272756, A
113	33	58.9	390	4	US-10-437-963-162185	Sequence 162185, A	186	32	57.1	294	5	US-10-617-320-4325	Sequence 4325, Ap
114	33	58.9	401	4	US-10-369-493-13094	Sequence 13094, A	187	32	57.1	295	4	US-10-238-075-1067	Sequence 1067, Ap
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116	33	58.9	417	4	US-10-724-972A-4231	Sequence 4231, Ap	189	32	57.1	296	4	US-10-238-075-893	Sequence 893, App
117	33	58.9	436	5	US-10-450-763-60727	Sequence 60727, Ap	190	32	57.1	323	4	US-10-437-963-103031	Sequence 103031, A
118	33	58.9	446	4	US-10-437-963-162181	Sequence 162181, A	191	32	57.1	329	6	US-11-014-968-4	Sequence 4, Appl1
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120	33	58.9	462	4	US-10-369-493-13442	Sequence 13442, A	193	32	57.1	333	4	US-10-072-012-747	Sequence 747, App
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147	32	57.1	67	4	US-10-425-115-254509	Sequence 254509, A	220	32	57.1	592	6	US-11-106-649-222	Sequence 36672, A
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151	32	57.1	104	5	US-10-719-993-444	Sequence 444, App	224	32	57.1	641	4	US-10-437-963-181519	Sequence 181519, A
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153	32	57.1	107	3	US-09-738-626-6786	Sequence 6786, Ap	226	32	57.1	707	4	US-10-282-122A-46469	Sequence 6187, Ap
154	32	57.1	107	4	US-10-781-014-672	Sequence 672, App	227	32	57.1	720	4	US-11-106-698-6187	Sequence 37860, A
155	32	57.1	115	4	US-10-424-599-188640	Sequence 188640, A	228	32	57.1	739	6	US-10-437-963-110813	Sequence 110813, A
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157	32	57.1	128	4	US-10-425-114-54977	Sequence 54977, A	230	32	57.1	811	4	US-10-408-765A-797	Sequence 797, App
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160	32	57.1	143	4	US-10-767-701-53614	Sequence 53614, A	233	32	57.1	909	4	US-10-369-493-12826	Sequence 12826, A
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165	32	57.1	154	3	US-09-975-456B-8	Sequence 8, Appl1	238	32	57.1	1067	4	US-10-369-493-2079	Sequence 2079, Ap
166	32	57.1	154	4	US-10-425-115-363550	Sequence 363550, A	239	32	57.1	1178	4	US-10-369-493-21939	Sequence 21939, A
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173	32	57.1	197	4	US-10-425-115-315829	Sequence 315829, A	246	32	57.1				

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:28:34 ; Search time 64.625 Seconds
(without alignments)
71.120 Million cell updates/sec

Title: US-10-091-135-10
Perfect score: 56
Sequence: 1 LTGSTAAKYDD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	56	100.0	202	4	US-10-001-245-117
5	56	100.0	203	4	US-10-001-245-118
6	56	100.0	204	3	US-09-847-208-162
7	56	100.0	204	4	US-10-091-135-16
8	56	100.0	204	4	US-10-091-135-65
9	56	100.0	204	4	US-10-091-135-81
10	56	100.0	204	4	US-10-091-135-39
11	56	100.0	209	3	US-09-957-806A-22
12	56	100.0	210	4	US-10-001-245-214
13	56	100.0	227	3	US-09-847-208-170
14	56	100.0	227	5	US-10-809-669-82
15	56	100.0	227	5	US-09-847-208-163
16	51	91.1	204	3	US-09-847-208-163
17	51	91.1	204	4	US-10-091-135-67
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19	45	80.4	204	3	US-09-847-208-166
20	45	80.4	204	4	US-10-091-135-66
21	44	78.6	204	3	US-09-847-208-165
22	44	78.6	204	4	US-10-091-135-63
23	40	71.4	214	5	US-10-450-763-53985
24	38	67.9	628	4	US-10-437-963-181903
25	37	66.1	171	5	US-10-450-763-42507
26	37	66.1	412	3	US-09-741-669-331
27	37	66.1	412	4	US-10-282-122A-42736

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91	62.5	35	36	4	US-10-425-114-45290	Sequence 45290, A
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145	62.5	35	38	4	US-10-437-963-163386	Sequence 163386, A
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145	62.5	35	40	4	US-10-425-115-222487	Sequence 222487, A
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145	62.5	35	43	4	US-10-425-115-224235	Sequence 224235, A
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179	62.5	35	45	4	US-10-425-114-52113	Sequence 52113, A
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422	62.5	35	51	5	US-10-472-928-2146	Sequence 2146, Ap
486	62.5	35	52	5	US-10-617-320-4823	Sequence 4823, Ap
528	62.5	35	53	4	US-11-097-143-32391	Sequence 32391, A
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468	60.7	34	73	4	US-10-369-493-8328	Sequence 8328, Ap
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123	58.9	33	92	5	US-10-450-763-56557	Sequence 275042, A
136	58.9	33	93	4	US-10-424-599-275042	Sequence 147748, A
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178	58.9	33	96	4	US-10-032-201B-52	Sequence 280573, A
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182	58.9	33	98	4	US-10-032-201B-54	Sequence 54875, A
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183	58.9	33	100	4		

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102	31	55.4	467	2	US-09-758-759-107	Sequence 107, App	175	30	53.6	389	2	US-09-055-765-15	Sequence 15, Appl
103	31	55.4	513	2	US-09-543-681A-4981	Sequence 1981, Ap	176	30	53.6	389	2	US-10-036-507-15	Sequence 15, Appl
104	31	55.4	514	2	US-09-489-039A-10028	Sequence 10028, A	177	30	53.6	389	2	US-10-197-220-112	Sequence 112, App
105	31	55.4	523	2	US-09-489-039A-14269	Sequence 14269, A	178	30	53.6	391	2	US-09-198-452A-737	Sequence 737, App
106	31	55.4	568	2	US-09-134-001C-3768	Sequence 3768, Ap	179	30	53.6	394	2	US-09-191-606-15	Sequence 15, Appl
107	31	55.4	615	2	US-09-198-452A-1037	Sequence 1037, App	180	30	53.6	394	2	US-09-438-185A-697	Sequence 697, App
108	31	55.4	615	2	US-09-438-185A-967	Sequence 967, App	181	30	53.6	400	2	US-09-489-039A-11075	Sequence 11075, A
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115	31	55.4	846	2	US-10-072-841A-33	Sequence 33, Appl	188	30	53.6	428	2	US-09-252-991A-26833	Sequence 26833, A
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125	30	53.6	17	2	US-09-709-201B-93	Sequence 93, Appl	198	30	53.6	565	2	US-08-951-742-8	Sequence 8, Appl
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131	30	53.6	76	2	US-09-882-434A-16	Sequence 16, Appl	204	30	53.6	660	2	US-09-976-594-787	Sequence 787, App
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135	30	53.6	76	2	US-09-882-434A-20	Sequence 20, Appl	208	30	53.6	662	2	US-09-744-125-6	Sequence 5627, Ap
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139	30	53.6	142	2	US-10-088-092A-15	Sequence 15, Appl	212	30	53.6	716	2	US-09-402-936-5	Sequence 5, Appl
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147	30	53.6	249	2	US-09-270-767-40272	Sequence 40272, A	220	30	53.6	942	1	US-08-141-324-14	Sequence 14, Appl
148	30	53.6	249	2	US-09-270-767-55488	Sequence 55488, A	221	30	53.6	942	1	US-08-541-902-14	Sequence 14, Appl
149	30	53.6	256	2	US-09-270-767-45809	Sequence 45809, A	222	30	53.6	959	2	US-09-107-433-4334	Sequence 4334, Ap
150	30	53.6	282	2	US-09-544-618-12	Sequence 12, Appl	223	30	53.6	1032	2	US-09-583-110-3366	Sequence 3366, Ap
151	30	53.6	282	2	US-09-544-618-17	Sequence 17, Appl	224	30	53.6	1177	2	US-09-134-001C-5106	Sequence 5106, Ap
152	30	53.6	282	2	US-09-544-618-18	Sequence 18, Appl	225	30	53.6	1186	2	US-09-248-796A-16183	Sequence 16183, A
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164	30	53.6	322	2	US-09-602-777A-308	Sequence 308, App	237	30	53.6	1732	2	US-09-479-467A-15	Sequence 15, Appl
165	30	53.6	335	2	US-09-252-991A-27013	Sequence 27013, A	238	30	53.6	2870	2	US-09-655-160-15	Sequence 15, Appl
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170	30	53.6	353	2	US-09-489-039A-8090	Sequence 8090, Ap	243	29	51.8	68	2	US-09-134-001C-3065	Sequence 3065, Ap
171	30	53.6	356	2	US-08-765-307A-8	Sequence 8, Appl	244	29	51.8	68	2	US-09-967-869A-5	Sequence 5, Appl
172	30	53.6	356	2	US-09-987-614A-8	Sequence 8, Appl	245	29	51.8	89	2	US-09-819-930-2	Sequence 2, Appl
173	30	53.6	367	2	US-09-391-606-16	Sequence 16, Appl	246	29	51.8	89	2		

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

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Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	35	62.5	419	2	US-09-240-936-2 Sequence 3765, Ap
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13	35	62.5	914	2	US-10-043-418-2 Sequence 4, Appli
14	34	60.7	89	2	US-09-819-930-4 Sequence 3757, Ap
15	34	60.7	304	2	US-09-583-110-3757 Sequence 4375, Ap
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20	34	60.7	682	1	US-08-441-139-2 Sequence 4, Appli
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93	31	55.4	310	2	US-09-248-796A-17322 Sequence 17322, A
94	31	55.4	314	2	US-09-902-540-16620 Sequence 16620, A
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96	31	55.4	354	2	US-09-903-540-12566 Sequence 12566, A
97	31	55.4	376	2	US-09-489-039A-9731 Sequence 9731, Ap
98	31	55.4	385	2	US-09-328-352-6804 Sequence 6804, Ap
99	31	55.4	417	2	US-09-248-796A-17934 Sequence 17934, A
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117	35	62.5	828	2	Q5VNL	HUMAN	Q5vv18	homo sapien	190	34	60.7	399	2	Q5HEL9	STAAC	Q5hel9	staphylococ	
118	35	62.5	850	2	Q4IB18	GIBZE	Q4ib18	giberella	191	34	60.7	399	2	Q7A4Q6	STAAN	Q7a4q6	staphylococ	
119	35	62.5	913	1	AGLU	BETU	Q04931	beta vulgar	192	34	60.7	399	2	Q99SY4	STAAN	Q99sy4	staphylococ	
120	35	62.5	952	1	ATGI	BOTCI	Q6h911	botrytis ci	193	34	60.7	400	2	Q631J7	BURPS	Q631j7	burkholderi	
121	35	62.5	956	2	Q6CQ49	KIULA	Q6cq49	kluyveromyc	194	34	60.7	401	2	Q8L313	STAAN	Q8l313	staphylococ	
122	35	62.5	1011	2	Q6CF27	YARLI	Q6cf27	yarrowia li	195	34	60.7	401	2	Q5X4W2	LEGPA	Q5x4w2	legionella	
123	35	62.5	1135	2	Q4TUY8	SUCHONG	Q4tuy8	suchong vir	196	34	60.7	412	2	Q4L614	STAAN	Q4l614	staphylococ	
124	35	62.5	1135	2	Q4TUY9	SUCHONG	Q4tuy9	suchong vir	197	34	60.7	442	1	GLXD	RHIME	Q87392	staphylococ	
125	35	62.5	1162	2	Q9LPQ7	ARATH	Q9lpq7	arabidopsis	198	34	60.7	442	2	Q986L0	RHIL0	Q986l0	rhizobium	l
126	35	62.5	1216	2	Q527R4	MAGR	Q527r4	magnaporthie	199	34	60.7	442	2	Q8U870	AGRT5	Q8u870	agrobacteri	
127	35	62.5	1263	2	Q8IK49	PLAF7	Q8ik49	plasmodium	200	34	60.7	449	2	Q8DFK6	VIBVU	Q8dfk6	vibriu vuln	
128	35	62.5	1284	2	Q4XXG5	PLACH	Q4xxg5	plasmodium	201	34	60.7	466	1	SVC	BAGSU	Q06752	bacillus eu	
129	35	62.5	1574	1	SYNJ1	RAT	Q62910	rattus norv	202	34	60.7	470	1	MOT4	MOUSE	P57787	mus musculu	
130	35	62.5	1690	2	Q8T9E7	DROME	Q8t9e7	drosofila	203	34	60.7	471	2	Q6AQ10	DESPP	Q6aq10	desulfocale	
131	35	62.5	2096	1	HEATR	DROME	Q8t9e7	drosofila	204	34	60.7	486	2	Q6FTB9	CANGA	Q6ftb9	candida gla	
132	35	62.5	2096	2	Q6AWS0	DROME	Q6aw50	drosofila	205	34	60.7	500	2	Q82K77	STRAW	Q82k77	streptomyce	
133	34	60.7	46	1	Y504	TREPA	Q831z1	treponema	206	34	60.7	506	2	Q73TF5	MYCPA	Q73tf5	mycobacteri	
134	34	60.7	57	2	Q5L1Z1	BACFN	Q5l1z1	bacteroides	207	34	60.7	507	2	Q6LGG2	PHOPR	Q6lgg2	photobacter	
135	34	60.7	159	2	Q5X832	LEGPA	Q5x832	legionella	208	34	60.7	509	2	Q4PG14	USTMA	Q4pg17	ustilago	ma
136	34	60.7	160	1	RT10	MOUSE	Q802k0	mus musculu	209	34	60.7	554	1	MBD4	MOUSE	Q92zd7	mus musculu	
137	34	60.7	160	2	Q4V9W5	MOUSE	Q4v9w5	mus musculu	210	34	60.7	556	1	GLI1	CHICK	P55978	gallus gall	
138	34	60.7	162	2	Q5ZYL6	LEGPH	Q5zyl6	legionella	211	34	60.7	579	2	Q7MVT5	PORGI	Q7mvt5	porphyromon	
139	34	60.7	174	2	Q8G3L0	BIFLO	Q8g3l0	bifidobacte	212	34	60.7	581	2	Q8ZYM0	PYRAE	Q8zym0	pyrobaculum	
140	34	60.7	192	2	Q50LJ4	MOUSE	Q50lj4	mus musculu	213	34	60.7	586	2	Q9CMW6	PASMU	Q9cmw6	pasteurella	
141	34	60.7	259	2	Q9HKA8	THEAC	Q9hka8	thermoplasma	214	34	60.7	612	2	Q6MIJ2	BEBEA	Q6mi12	bdellovibri	
142	34	60.7	272	2	Q9RTJ1	STROCO	Q9rtj1	streptomyce	215	34	60.7	613	2	Q82EQ0	STRAW	Q82eq0	streptomyce	
143	34	60.7	281	2	Q8TGH1	9HYPO	Q8tgh1	cordyceps	216	34	60.7	622	2	Q62S26	BACLD	Q62s26	bacillus li	
144	34	60.7	281	2	Q8TF95	9HYPO	Q8tf95	cordyceps	217	34	60.7	633	2	Q65HJ2	BACLD	Q65hj2	saccharomyc	
145	34	60.7	281	2	Q8TF99	9HYPO	Q8tf99	cordyceps	218	34	60.7	682	1	GRF78	YEAST	Q97fr9	clostridium	
146	34	60.7	284	2	Q4IAD6	GIBZE	Q4iad6	giberella	219	34	60.7	696	2	Q97FR5	CLOAB	Q97fr5	clostridium	
147	34	60.7	286	2	Q727F6	DESUVH	Q727f6	desulfovibr	220	34	60.7	697	2	Q8EB65	SHON	Q8eb65	shewanella	
148	34	60.7	290	2	Q88DP9	PSEPK	Q88dp9	pseudomonas	221	34	60.7	705	2	Q8XTL2	RALSO	Q8xtl2	ralstonia	s
149	34	60.7	291	2	Q5G598	MAGR	Q5g598	magnaporthie	222	34	60.7	720	2	Q5A7N2	CANAL	Q5a7n2	candida alb	
150	34	60.7	291	2	Q61K06	CASER	Q61k06	caenorhabdi	223	34	60.7	726	2	Q72CM5	DESUVH	Q72cm5	desulfovibr	
151	34	60.7	296	2	Q5IOA0	SHIBO	Q5ioa0	shigella	224	34	60.7	756	2	Q8DKB1	SYNEL	Q8dkb1	synecococc	
152	34	60.7	298	2	Q62415	CABEL	Q62415	caenorhabdi	225	34	60.7	764	2	Q8XTM0	RALSO	Q8xtm0	ralstonia	s
153	34	60.7	311	1	MCH	HALSA	Q9hpd7	halobacteri	226	34	60.7	787	2	Q6CPG2	KIULA	Q6cp3	kluyveromyc	
154	34	60.7	318	2	Q5XJ57	BRARE	Q5xj57	brachydanio	227	34	60.7	788	1	TSR1	YEAST	Q07381	saccharomyc	
155	34	60.7	319	2	Q93PS4	COMTE	Q93ps4	comamonas	228	34	60.7	818	2	Q5F8S5	NRIG1	Q5f8s5	neisseria	g
156	34	60.7	323	2	Q6TR99	METAN	Q6tr99	metarhizium	229	34	60.7	857	2	Q8H9R1	9CAUD	Q8h9r1	vibrio harv	
157	34	60.7	323	2	Q6TR98	METAN	Q6tr98	metarhizium	230	34	60.7	861	2	Q4IP83	GIBZE	Q4ip83	giberella	
158	34	60.7	323	2	Q6TR97	METAN	Q6tr97	metarhizium	231	34	60.7	863	2	Q8XPQ3	RALSO	Q8xpq3	ralstonia	s
159	34	60.7	323	2	Q6TR96	METAN	Q6tr96	metarhizium	232	34	60.7	869	2	Q4PD70	USTMA	Q4pd70	ustilago	ma
160	34	60.7	323	2	Q6TR95	METAN	Q6tr95	metarhizium	233	34	60.7	900	2	Q7P8H2	FUSNV	Q7p8h2	fusobacteri	
161	34	60.7	323	2	Q6TR94	METAN	Q6tr94	metarhizium	234	34	60.7	902	2	Q22444	ARATH	Q22444	arabidopsis	
162	34	60.7	323	2	Q6TR93	METAN	Q6tr93	metarhizium	235	34	60.7	902	2	Q22444	ARATH	Q22444	arabidopsis	
163	34	60.7	323	2	Q6TR92	METAN	Q6tr92	metarhizium	236	34	60.7	926	2	Q515D5	9TELE	Q515d5	aplysia cal	
164	34	60.7	323	2	Q6TR91	METAN	Q6tr91	metarhizium	237	34	60.7	928	2	Q515D5	9TELE	Q515d5	aplysia cal	
165	34	60.7	323	2	Q6TR90	METAN	Q6tr90	metarhizium	238	34	60.7	943	2	Q89E4	PSESM	Q89e4	pseudomonas	
166	34	60.7	323	2	Q6TR89	METAN	Q6tr89	metarhizium	239	34	60.7	954	2	Q8ZB21	YERPE	Q8zb21	yersinia pe	
167	34	60.7	323	2	Q6TR88	METAN	Q6tr88	metarhizium	240	34	60.7	963	2	Q8D1M6	YERPE	Q8d1m6	yersinia pe	
168	34	60.7	323	2	Q6TR87	METAN	Q6tr87	metarhizium	241	34	60.7	970	2	Q4H8Y3	9BEO	Q4h8y3	delnecococc	
169	34	60.7	323	2	Q6TR86	METAN	Q6tr86	metarhizium	242	34	60.7	1063	1	XPO1	DROME	Q9v45	drosofila	
170	34	60.7	323	2	Q6TR85	METAN	Q6tr85	metarhizium	243	34	60.7	1169	2	Q9VX45	DROME	Q9vx45	drosofila	
171	34	60.7	323	2	Q6TR84	METAN	Q6tr84	metarhizium	244	34	60.7	1174	2	Q8MQX9	DROME	Q8mqx9	candida alb	
172	34																	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 115.958 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-10
Perfect score: 56
Sequence: 1 LTGSTAAKYDD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05_80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	204	1 VA5_VESFU	P35783 vespula fla
2	56	100.0	227	1 VA5_VESFU	Q05110 vespula vul
3	51	91.1	204	1 VA5_VESGE	P35784 vespula ger
4	45	80.4	204	1 VA5_VESPE	P35785 vespula pen
5	44	78.6	204	1 VA5_VESMC	P35760 vespula mac
6	41	73.2	309	2 Q428U5 THAAR	Q428u5 thauera aro
7	41	73.2	309	2 Q428U6 9RHO	Q428u6 thauera chl
8	41	73.2	309	2 Q428U8 THAAR	Q428u8 thauera aro
9	41	73.2	309	2 Q428U9 THAAR	Q428u9 thauera chl
10	41	73.2	309	2 Q428V0 9RHO	Q428v0 thauera chl
11	41	73.2	386	2 Q428U4 THAAR	Q428u4 thauera aro
12	40	71.4	787	2 Q9RSU0 DEIRA	Q86sa8 porcellio d
13	39	69.6	146	1 AGH_PORDI	Q41l18 lactobacill
14	39	69.6	487	2 Q4JL18 LACRE	Q9cca5 nephroselm
15	38	67.9	189	2 Q9TCA5_NEPOL	Q53r46 cryptococcu
16	38	67.9	284	2 Q5SR46 CRYNE	Q5Kf23 cryptococcu
17	38	67.9	284	2 Q5Kf23 CRYNE	Q428u4 thauera ael
18	38	67.9	309	2 Q428U4 THASE	Q428u4 thauera chl
19	38	67.9	533	2 Q4RPR4 TETNG	Q428u4 thauera chl
20	38	67.9	685	2 Q4RW7 TETNG	Q428u4 thauera chl
21	38	67.9	985	1 SMCL_ARATH	Q8vy05 arabidopsis
22	37	66.1	165	2 Q6ZNX5 HUMAN	Q6znx5 homo sapien
23	37	66.1	207	2 Q4UM07 RICFE	Q4um07 rickettsia
24	37	66.1	242	2 Q7PBK2 RICSI	Q7pbk2 rickettsia
25	37	66.1	242	2 Q92ID7 RICCN	Q92id7 rickettsia
26	37	66.1	309	2 Q428U7 9RHO	Q428u7 thauera chl
27	37	66.1	342	2 Q98I05 RHIL0	Q98i05 rhizobium 1
28	37	66.1	412	1 YACD_ECOLI	P31058 escherichia
29	37	66.1	476	1 YCTB_SCHPO	P78813 schizosacch
30	37	66.1	480	2 Q8C3E8 MOUSE	Q8c3e8 mus musculu
31	37	66.1	708	2 Q7NK89_GLOVI	Q7nk89 gloebacter

32	37	66.1	718	2	Q4HD17_9DEIO	Q4hd17 deinococcus
33	37	66.1	744	2	Q928H5_LISIN	Q928h5 listeria in
34	37	66.1	744	2	Q8Y4H8_LISMO	Q8y4h8 listeria mo
35	37	66.1	841	2	Q7VCB3_PROMA	Q7vcb3 prochloroco
36	37	66.1	1724	2	Q4RMC8_TETNG	Q4rmc8 tetraodon n
37	37	66.1	5183	2	Q8TDN5_HUMAN	Q8tdn5 homo sapien
38	37	66.1	5183	2	Q5T4S7_HUMAN	Q5t4s7 homo sapien
39	36	64.3	74	2	Q84235_ORYSA	Q84235 oryza sativ
40	36	64.3	102	1	CCAC_AMPCA	P55738 amphidinum
41	36	64.3	142	2	Q82DR7_STRAW	Q82dr7 streptomyc
42	36	64.3	142	2	Q5U039_MIMIV	Q5u039 mimivirus.
43	36	64.3	193	2	Q8KY43_STRCO	Q8ky43 streptomyc
44	36	64.3	193	2	Q82B77_STRAW	Q82b77 streptomyc
45	36	64.3	250	2	Q422M6_PLABE	Q422m6 plasmodium
46	36	64.3	260	1	NQRC_VIBHA	Q9rfv9 vibrio harv
47	36	64.3	294	2	Q8PVU4_METMA	Q8pvu4 methanosarc
48	36	64.3	299	1	PUR7_STRCO	Q9rk11 streptomyc
49	36	64.3	299	2	Q66G03_PLOIN	Q66g03 plodia inte
50	36	64.3	352	2	Q6ANR4_DESPS	Q6anr4 deulifotale
51	36	64.3	465	2	Q85G88_CYAME	Q85g88 cyanidiosch
52	36	64.3	516	1	PUR9_COREF	Q8frx6 c bifunctio
53	36	64.3	521	1	PUR9_COREF	Q8fr29 c bifunctio
54	36	64.3	524	2	Q8CJ56_STRCO	Q8cj56 streptomyc
55	36	64.3	525	2	Q6NID8_CORDI	Q6nij8 corynebacte
56	36	64.3	721	2	Q8PA53_XANCP	Q8pas3 xanthomonas
57	36	64.3	781	2	Q4LWK6_9BURK	Q4lwk6 burkholderi
58	36	64.3	799	2	Q5KMB5_CRYNE	Q5kmb5 cryptococcu
59	36	64.3	799	2	Q5XM0_CRYNE	Q5xm0 cryptococcu
60	36	64.3	820	2	Q76182_AMPCA	Q76182 amphidinum
61	36	64.3	957	2	Q93781_CAEEL	Q93781 caenorhabdi
62	36	64.3	996	2	Q55HA2_CRYNE	Q55ha2 cryptococcu
63	36	64.3	996	2	Q5K6V8_CRYNE	Q5k6v8 cryptococcu
64	36	64.3	1350	2	Q95Y18_9APIC	Q95y18 plasmodium
65	36	64.3	1350	2	Q7RBM4_PLAYO	Q7rbm4 plasmodium
66	36	64.3	1361	2	Q30524_WOLRE	Q30524 wolinnella r
67	36	64.3	1361	2	Q87083_WOLRE	Q87083 wolinnella r
68	36	64.3	1372	1	COLA2_MOUSE	Q01149 mus musculu
69	36	64.3	1372	1	COLA2_RAT	P02466 rattus norv
70	36	64.3	1465	2	Q4UT11_XANCP	Q4ut11 xanthomonas
71	36	64.3	4210	2	Q89J13_BRAJA	Q89j13 bradyrhizob
72	35	62.5	130	2	Q98IT9_RHIL0	Q98it9 rhizobium 1
73	35	62.5	145	2	Q9AY76_ORYSA	Q9ay76 oryza sativ
74	35	62.5	197	1	NDOC_RICPR	Q9zd3h rickettsia
75	35	62.5	197	1	Q68X18_RICTY	Q68x18 rickettsia
76	35	62.5	203	2	Q8SR11_ENCCU	Q8sr11 encephalito
77	35	62.5	206	2	Q52DK2_WAGGR	Q52dk2 magnaporthe
78	35	62.5	240	2	Q8JM50_9NUCL	Q8jm50 mamestra co
79	35	62.5	266	2	Q7ULC7_RHOBA	Q7ulc7 rhodopirell
80	35	62.5	272	2	Q4T673_TETNG	Q4t673 tetraodon n
81	35	62.5	299	2	Q4RIK1_TETNG	Q4rik1 tetraodon n
82	35	62.5	311	2	Q27783_METTH	Q27783 methanobact
83	35	62.5	319	2	Q5G1K1_9BURK	Q5g1k1 comamonas s
84	35	62.5	319	2	Q75T27_PSEOC	Q75t27 pseudomonas
85	35	62.5	335	2	Q80LQ4_NPVAH	Q80lq4 adoxophyas
86	35	62.5	347	2	Q9PHU0_XYLFA	Q9phj0 xyella fas
87	35	62.5	368	2	Q6LBB6_OLICA	Q6lbb6 oligotropha
88	35	62.5	369	2	Q7S111_NEUCR	Q7s111 neuropept
89	35	62.5	390	2	Q5ZPB4_9DELT	Q5zpb4 angiococcus
90	35	62.5	396	1	EFTU_CACR	Q5zpb4 angiococcus
91	35	62.5	399	2	Q6A8S9_PROAC	Q6a8s9 caulobacter
92	35	62.5	403	2	Q89S27_BRAJA	Q89s27 bradyrhizob
93	35	62.5	419	1	MURA2_STRPN	Q89s27 bradyrhizob
94	35	62.5	419	1	MURA2_STRPN	Q89s27 bradyrhizob
95	35	62.5	440	2	Q51T87_WAGGR	Q51t87 magnaporthe
96	35	62.5	449	2	Q625A2_CACBR	Q625a2 caenorhabdi
97	35	62.5	453	2	Q7UES2_RHOBA	Q7ues2 rhodopirell
98	35	62.5	471	1	MOT4_RAT	Q35910 rattus norv
99	35	62.5	476	2	Q4MV79_BACCE	Q4mv79 bacillus ce
100	35	62.5	489	2	Q8IK65_PLAF7	Q8ik65 plasmodium
101	35	62.5	504	2	Q4R7J5_WACFA	Q4r7j5 macaca fasc
102	35	62.5	541	1	LNT_BORPA	P61033 bordetella
103	35	62.5	547	1	LNT_BORBR	Q7wmn7 bordetella
104	35	62.5	547	1	LNT_BORPE	P61034 bordetella

103	32	57.1	295	2	F90938	hypothetical prote	176	31	55.4	226	2	H84213	hypothetical prote
104	32	57.1	295	2	B85664	transposase for IS	177	31	55.4	234	2	T49448	hypothetical prote
105	32	57.1	295	2	D90801	hypothetical prote	178	31	55.4	242	2	A86189	protein T2N20.7 [
106	32	57.1	295	2	B85613	probable transposa	179	31	55.4	265	2	C70963	hypothetical prote
107	32	57.1	295	2	B85787	probable transposa	180	31	55.4	269	2	S16671	Dd31 protein - sli
108	32	57.1	295	2	T00315	transposase - Esch	181	31	55.4	283	2	A35935	NADH2 dehydrogenas
109	32	57.1	295	2	B85661	probable transposa	182	31	55.4	316	2	G97148	malonyl CoA-acyl c
110	32	57.1	296	2	A85698	transposase for IS	183	31	55.4	327	2	AG0870	hypothetical prote
111	32	57.1	296	2	A99840	transposase - Esch	184	31	55.4	337	2	AH2591	membrane lipoprote
112	32	57.1	296	2	167971	probable transposa	185	31	55.4	337	2	B97374	Deinococcus radiol
113	32	57.1	296	2	A85841	hypothetical prote	186	31	55.4	338	2	T49998	hypothetical prote
114	32	57.1	296	2	D91284	hypothetical prote	187	31	55.4	345	2	E84398	phosphate ABC tran
115	32	57.1	296	2	F90868	hypothetical prote	188	31	55.4	350	2	A82299	outer membrane pro
116	32	57.1	296	2	D90995	hypothetical prote	189	31	55.4	383	2	AG3312	x-Pro dipeptidase
117	32	57.1	296	2	E91020	hypothetical prote	190	31	55.4	385	2	G87006	probable transmemb
118	32	57.1	296	2	F91111	hypothetical prote	191	31	55.4	394	2	F86190	hypothetical prote
119	32	57.1	296	2	G90998	hypothetical prote	192	31	55.4	398	2	T33446	hypothetical prote
120	32	57.1	296	2	T00240	transposase - Esch	193	31	55.4	399	2	S75862	translation elonga
121	32	57.1	296	2	E90837	hypothetical prote	194	31	55.4	399	2	E71169	hypothetical prote
122	32	57.1	296	2	C91065	hypothetical prote	195	31	55.4	401	2	A13568	mannonate dehydrat
123	32	57.1	296	2	H90779	hypothetical prote	196	31	55.4	401	2	E82521	hypothetical prote
124	32	57.1	296	2	C90906	hypothetical prote	197	31	55.4	407	2	S76637	conserved hypotet
125	32	57.1	296	2	A99972	hypothetical prote	198	31	55.4	411	2	A12939	hypothetical prote
126	32	57.1	296	2	C90978	hypothetical prote	199	31	55.4	411	2	F98342	probable flagella-
127	32	57.1	296	2	H85824	IS629 transposase	200	31	55.4	419	2	G75062	hypothetical prote
128	32	57.1	296	2	S09261	probable transposa	201	31	55.4	435	2	AD3236	htrA-like protein
129	32	57.1	296	2	JC4309	glyceraldehyde-3-p	202	31	55.4	435	2	T22777	proteinase DO (EC
130	32	57.1	333	2	TWMSFB	transforming prote	203	31	55.4	474	1	I40059	MFS permease (impo
131	32	57.1	338	1	S34153	mat101-1 protein -	204	31	55.4	474	2	A13349	hypothetical 51.5k
132	32	57.1	344	2	B69102	hypothetical prote	205	31	55.4	475	2	AG3652	hypothetical 51.5k
133	32	57.1	355	2	E96591	hypothetical prote	206	31	55.4	475	2	D97434	conserved hypotet
134	32	57.1	426	2	E83620	probable amidase p	207	31	55.4	475	2	AE0855	probable 4-hydroxy
135	32	57.1	485	2	H87438	tryptophan halogen	208	31	55.4	475	2	H91077	probable 4-hydroxy
136	32	57.1	503	2	F70813	hypothetical prote	209	31	55.4	475	2	T44997	NADH dehydrogenase
137	32	57.1	504	2	T25424	hypothetical prote	210	31	55.4	475	2	A85923	outer capsid prote
138	32	57.1	548	2	A11395	dipeptide ABC tran	211	31	55.4	500	2	AF3235	tubulin-like prote
139	32	57.1	553	2	AD1771	hypothetical prote	212	31	55.4	526	1	P5XRBT	H+-transporting tw
140	32	57.1	585	2	T48513	phassolin G-box bi	213	31	55.4	527	2	T04701	probable hydrolase
141	32	57.1	614	2	T10862	Glutamate-amonia	214	31	55.4	564	2	D85439	mycodextranase (EC
142	32	57.1	700	2	I40596	probable TonB-depe	215	31	55.4	574	2	S23530	lipid A disacchari
143	32	57.1	721	2	B83237	probable ABC trans	216	31	55.4	584	2	AI0673	lipid-A-disacchari
144	32	57.1	725	2	C84423	probable ABC trans	217	31	55.4	604	2	C86611	probable peptidase h
145	32	57.1	824	2	T36818	DNA-directed DNA p	218	31	55.4	604	2	B72014	GRP-binding elonga
146	32	57.1	898	1	D3BP74	hypothetical prote	219	31	55.4	604	2	AF1564	GRP-binding elonga
147	32	57.1	935	2	T16489	hypothetical prote	220	31	55.4	612	2	AC1208	dnak-type molecula
148	32	57.1	1005	2	C71513	hypothetical prote	221	31	55.4	612	2	AF1564	immune inhibitor A
149	32	57.1	1015	2	T41111	hypothetical App b	222	31	55.4	612	2	AC1208	hypothetical prote
150	32	57.1	1067	1	S62421	endopeptidase La h	223	31	55.4	612	2	AF1564	beta-lactamase cla
151	32	57.1	1178	1	QYBYP	pyruvate carboxyla	224	31	55.4	645	2	S41372	integrin beta chai
152	32	57.1	1253	2	T21065	suppressor of sabl	225	31	55.4	656	2	S51712	probable secreted
153	32	57.1	1473	2	T13855	zinc metalloprotei	226	31	55.4	656	2	S51712	vrIC protein - Dic
154	32	57.1	1881	2	H95076	variant-specific s	227	31	55.4	687	2	S12399	hypothetical prote
155	32	57.1	2135	2	T14602	cell wall-associat	228	31	55.4	714	2	T14080	hypothetical prote
156	32	57.1	2334	2	S32920	CPV protein - midg	229	31	55.4	714	2	T15306	beta-lactamase cla
157	32	57.1	3512	2	T17121	transcriptional regu	230	31	55.4	735	2	E97245	integrin beta chai
158	32	57.1	3512	2	T17121	transcriptional regu	231	31	55.4	865	2	A30889	probable secreted
159	31.5	56.2	280	2	H72389	hypothetical prote	232	31	55.4	875	2	T17382	vrIC protein - Dic
160	31.5	56.2	330	2	S70127	E2/NSI protein (CD	233	31	55.4	884	2	T40690	hypothetical prote
161	31	55.4	55	2	P00828	E2/NSI protein (CD	234	31	55.4	933	2	AD3309	hypothetical membr
162	31	55.4	55	2	P00827	thioredoxin [impor	235	31	55.4	933	2	D70661	probable membranep
163	31	55.4	104	2	E89885	hypothetical prote	236	31	55.4	962	2	T24866	hypothetical prote
164	31	55.4	126	2	C69776	hypothetical prote	237	31	55.4	971	2	C71808	type I restriction
165	31	55.4	135	2	H88663	protein C02B10.6 [238	31	55.4	993	2	B64695	conserved hypotet
166	31	55.4	145	2	T15058	photosystem I prot	239	31	55.4	1018	2	AG0703	probable oxidase [
167	31	55.4	153	2	H86034	hypothetical prote	240	31	55.4	1018	2	B90928	probable oxidase y
168	31	55.4	153	2	G91187	hypothetical prote	241	31	55.4	1018	2	F85776	conserved hypotet
169	31	55.4	153	2	S47817	alpha-pilin - Mora	242	31	55.4	1018	2	AH0293	probable iron-sulf
170	31	55.4	155	2	JL0071	NADH2 dehydrogenas	243	31	55.4	1023	2	G64926	probable iron-sulf
171	31	55.4	170	2	T35957	hypothetical prote	244	31	55.4	1037	2	B59430	carbamoyl-phosphat
172	31	55.4	195	2	S33861	hypothetical prote	245	31	55.4	1037	2	I40377	DNA-binding protei
173	31	55.4	196	2	H93144	hypothetical prote	246	31	55.4	1043	2	A56037	1-phosphatidylinos
174	31	55.4	197	2	E87491	NADH dehydrogenase	247	31	55.4	1093	2	T18275	cell division prot
175	31	55.4	216	2	H69221	hypothetical prote	248	31	55.4	1343	2	AF0611	cell division prot

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 18.3333 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-10
Perfect score: 56
Sequence: 1 LTGSTAAKYDD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	204	2 A44583	venom allergen ant
2	51	91.1	204	2 B44583	venom allergen ant
3	45	80.4	204	2 C44583	venom allergen ant
4	44	78.6	204	2 B37329	antigen 5 - easter
5	40	71.4	787	2 D75325	glutamine synthase
6	38	67.9	827	2 T04789	hypothetical prote
7	37	66.1	242	2 C37760	NADH2 dehydrogenas
8	37	66.1	359	2 T42524	hypothetical prote
9	37	66.1	412	2 G47336	yadC protein - Esc
10	37	66.1	476	2 T41619	hypothetical prote
11	37	66.1	744	2 AG1382	transport protein
12	37	66.1	744	2 AD1751	transport protein
13	36	64.3	172	2 S65487	light-harvesting c
14	36	64.3	1361	2 T03415	S-layer protein -
15	36	64.3	1373	1 A43291	collagen alpha 2(I
16	36	64.3	1785	2 T32595	hypothetical prote
17	35	62.5	197	2 E71692	NADH2 dehydrogenas
18	35	62.5	311	1 C69101	conserved hypothet
19	35	62.5	347	2 G82862	conjugal transfer
20	35	62.5	396	2 A87403	translation elonga
21	35	62.5	419	2 A95125	hypothetical prote
22	35	62.5	419	2 E97995	UDP-N-acetylglucos
23	35	62.5	632	2 F36544	hypothetical prote
24	35	62.5	669	2 B60336	probable aldehyde
25	35	62.5	913	2 J05463	alpha-glucosidase
26	35	62.5	1575	2 S68448	synaptotjanin, 170K
27	34	60.7	46	2 D71317	hypothetical prote
28	34	60.7	298	2 T36554	hypothetical prote
29	34	60.7	311	2 A84321	hypothetical prote

30	34	60.7	369	2 C97994	rNA polymerase eig
31	34	60.7	369	2 A95124	rNA polymerase eig
32	34	60.7	385	2 AH2169	ABC transport syst
33	34	60.7	388	1 S22387	cuticicle-degrading
34	34	60.7	399	2 F89978	conserved hypothet
35	34	60.7	442	2 A13075	glutamate synthase
36	34	60.7	442	2 H98210	glutamC protein [i
37	34	60.7	466	1 C53402	cysteine-tRNA liga
38	34	60.7	682	1 HHBYK2	dnak-type molecula
39	34	60.7	696	2 B97227	glutamine syntheta
40	34	60.7	788	2 S67595	hypothetical prote
41	34	60.7	902	2 T48531	alpha-glucosidase
42	34	60.7	954	2 A10438	probable exported
43	34	60.7	1188	2 S48861	gene ei protein -
44	34	60.7	2492	1 A44213	nonstructural poly
45	34	60.7	2492	1 C44213	nonstructural poly
46	34	60.7	2492	1 MNWVTD	hypothetical prote
47	33	58.9	112	2 G70855	hypothetical prote
48	33	58.9	125	2 E75624	thioredoxin f prec
49	33	58.9	182	2 T07837	NADH2 dehydrogenas
50	33	58.9	204	2 S78165	ribose 5-phosphate
51	33	58.9	218	2 AD0112	ribose 5-phosphate
52	33	58.9	219	2 AE0874	ribosephosphate is
53	33	58.9	219	2 A98102	ribose 5-phosphate
54	33	58.9	219	2 A65076	ribosephosphate is
55	33	58.9	219	2 E85947	hypothetical prote
56	33	58.9	238	2 H87299	probable membrane
57	33	58.9	239	2 S64324	probable transcrip
58	33	58.9	270	2 C83167	conserved hypothet
59	33	58.9	310	2 E75476	probable integral
60	33	58.9	330	2 T36695	Similar to NU27 [i
61	33	58.9	371	2 F96754	translation elonga
62	33	58.9	410	2 S04391	hypothetical prote
63	33	58.9	412	2 F89905	NAD(PAD)-dependent
64	33	58.9	417	2 A97083	NADH dehydrogenase
65	33	58.9	419	2 D86728	lytic murein trans
66	33	58.9	421	2 AG2587	hypothetical prote
67	33	58.9	421	2 G97369	hypothetical prote
68	33	58.9	531	2 S36537	L1 protein - human
69	33	58.9	714	2 AE1353	penicillin-binding
70	33	58.9	769	2 D86335	T20H2.6 protein -
71	33	58.9	847	2 A48228	beta-N-acetylhexos
72	33	58.9	869	2 S49844	probable membrane
73	33	58.9	1186	2 AD1300	Smc protein essent
74	33	58.9	1355	1 VGBE11	149K glycoprotein
75	33	58.9	1609	2 S44821	F44E2.4 protein -
76	33	58.9	2182	2 T14320	calcineurin inhibi
77	32.5	58.0	454	2 C82682	glutamate-cysteine
78	32	57.1	44	2 B39859	flavocytochrome c
79	32	57.1	73	2 JS0107	hypothetical 7.4K
80	32	57.1	97	1 BVECGS	chaperonin GroES -
81	32	57.1	97	2 C91269	chaperonin GroES [
82	32	57.1	97	2 A86110	chaperonin mopB [a
83	32	57.1	127	2 S49195	GCR 20 protein - f
84	32	57.1	136	2 H85909	partial probable t
85	32	57.1	144	2 H45725	probable transposa
86	32	57.1	149	2 D47169	flavocytochrome c,
87	32	57.1	158	2 T05007	hypothetical prote
88	32	57.1	196	2 D72129	maf protein CP0754
89	32	57.1	196	2 H86493	Mat-type protein [
90	32	57.1	206	2 T44469	transposase tnpC [
91	32	57.1	215	2 A85745	hypothetical prote
92	32	57.1	215	2 D85977	probable transposa
93	32	57.1	215	2 C85695	probable transposa
94	32	57.1	215	2 A85715	hypothetical prote
95	32	57.1	217	2 B90765	hypothetical prote
96	32	57.1	229	2 E85806	hypothetical prote
97	32	57.1	229	2 D90958	NADH-ubiquinone ox
98	32	57.1	250	2 E82821	hypothetical prote
99	32	57.1	250	2 T15415	hypothetical prote
100	32	57.1	288	2 F85818	hypothetical prote
101	32	57.1	290	2 C95012	hypothetical prote
102	32	57.1	290	2 F97883	L-serine ammonia-1

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 96.7083 Seconds
(without alignments)

49.977 Million cell updates/sec

Title: US-10-091-135-10

Perfect score: 56

Sequence: 1 LTGSTAKYDD 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	11	5	Aae28816 Vespula v
2	56	100.0	48	5	Aae28813 Vespula v
3	56	100.0	204	2	Aaw35688 Vespida an
4	56	100.0	204	2	Aay45217 Wild type
5	56	100.0	204	5	Abg66977 Wasp veno
6	56	100.0	204	5	Abg66983 Wasp veno
7	56	100.0	204	5	Abg67052 Wasp veno
8	56	100.0	204	5	Abg67104 Wasp veno
9	56	100.0	204	5	Abg67103 Wasp veno
10	56	100.0	204	5	Aae28820 Vespula v
11	56	100.0	209	4	Abm00031 Allergen
12	56	100.0	227	2	Aay25644 Vespula s
13	56	100.0	227	4	Aae13071 Vespula v
14	56	100.0	227	4	Aac34893 Wasp alle
15	44	78.6	204	2	Aaw35687 Vespida an
16	40	71.4	214	4	Abg23626 Novel hum
17	37	66.1	18	8	Adl93350 Anti-V5 a
18	37	66.1	171	4	Abg12148 Novel hum
19	37	66.1	412	4	Ag98283 Escherich
20	37	66.1	412	6	Abu14812 Protein e
21	37	66.1	744	5	Abb49954 Listeria
22	37	66.1	1136	5	Adj33677 Protein o
23	37	66.1	1137	4	Abg28828 Novel hum
24	37	66.1	5183	8	Ado44006 Amino aci

25	37	66.1	5183	9	ADx06154	Cyclin-de
26	36	64.3	315	8	ADT58851	Plant pol
27	36	64.3	587	7	ADL15066	Human adu
28	36	64.3	1372	7	ADE59683	Rat Prote
29	36	64.3	1372	7	ADD45148	Rat Prote
30	36	64.3	1372	7	ADD45604	Rat Prote
31	36	64.3	1372	7	ADE59687	Rat Prote
32	36	64.3	1372	7	ADD47529	Rat Prote
33	36	64.3	1373	5	ABBS7364	Murine pr
34	36	64.3	1373	9	ADW44460	Murine pr
35	36	64.3	1785	8	ADN24366	Bacterial
36	35	62.5	91	8	ADN24366	Bacterial
37	35	62.5	133	7	ADN75924	Plant ful
38	35	62.5	178	8	ADN89247	Plant ful
39	35	62.5	178	8	ADN89449	Plant ful
40	35	62.5	200	8	ADY23598	Plant ful
41	35	62.5	251	7	ADC95024	E. faeciu
42	35	62.5	410	4	AAU45865	Propionib
43	35	62.5	410	6	AAW42384	Propionib
44	35	62.5	419	2	AAW80613	S. pneumo
45	35	62.5	419	3	AAU91116	Streptoco
46	35	62.5	419	4	AAU37737	Streptoco
47	35	62.5	419	4	AAU01044	CFE 47 pr
48	35	62.5	419	5	AAU01497	S. pneumo
49	35	62.5	419	6	ABU46035	Protein e
50	35	62.5	419	8	ADK47251	Streptoco
51	35	62.5	422	8	ADR96188	Novel S.
52	35	62.5	422	9	AEA60058	Streptoco
53	35	62.5	422	9	ABE68533	Drosophil
54	35	62.5	486	4	ABE68533	Protein e
55	35	62.5	528	6	ABU23082	Wild-type
56	35	62.5	914	6	ABU63150	Wild-type
57	35	62.5	1574	7	ADE55582	Rat Prote
58	35	62.5	2096	4	ABE65242	Drosophil
59	35	62.5	2096	8	ADQ89606	Antagonis
60	34	60.7	19	9	ADZ69708	Murine me
61	34	60.7	159	2	AAU11201	S. pneumo
62	34	60.7	171	9	ABE41846	L. pneumo
63	34	60.7	171	9	ABE38607	L. pneumo
64	34	60.7	174	5	ABP66316	Bifidobac
65	34	60.7	329	8	ADK47242	Streptoco
66	34	60.7	329	8	ADR95740	Novel S.
67	34	60.7	329	9	AEA59610	Streptoco
68	34	60.7	369	6	ABU01488	S. pneumo
69	34	60.7	369	6	ABU46032	Protein e
70	34	60.7	369	8	ADH97012	S. pneumo
71	34	60.7	369	8	ADH97014	S. pneumo
72	34	60.7	369	9	ABE13367	Streptoco
73	34	60.7	369	9	ABE13369	Streptoco
74	34	60.7	388	2	AAU42435	Cuticle-d
75	34	60.7	401	6	ABM71468	Staphyloc
76	34	60.7	401	9	ABE40964	L. pneumo
77	34	60.7	423	9	ABE37653	L. pneumo
78	34	60.7	468	8	ADN25675	Bacterial
79	34	60.7	682	4	AAU70749	S. cerevis
80	34	60.7	682	6	ABR52837	Protein e
81	34	60.7	682	7	ADK62272	Disease t
82	34	60.7	682	8	ADS43737	Bacterial
83	34	60.7	696	6	ABU24188	Protein e
84	34	60.7	788	6	ABR53137	Protein e
85	34	60.7	788	7	ADK63098	Disease t
86	34	60.7	788	8	ADT87236	Yeast Str
87	34	60.7	831	6	ABP78978	N. gonorr
88	34	60.7	902	6	ABU63302	Wild-type
89	34	60.7	927	6	ABU41568	Protein e
90	34	60.7	954	6	ABU50458	Protein e
91	34	60.7	1060	4	ABE68109	Drosophil
92	34	60.7	1169	4	ABE63860	Drosophil
93	34	60.7	1169	4	ABE63867	Drosophil
94	34	60.7	1169	7	ADK11389	Drosophil
95	34	60.7	1169	7	ADK11387	Drosophil
96	34	60.7	2492	5	AAE18302	Venezuela
97	34	60.7	2492	5	ADY26147	Venezuela

99	32	53.3	486	7	US-11-188-298-3455	Sequence 3455, Ap	172	31	51.7	246	7	US-11-290-153-436	Sequence 436, App
100	32	53.3	486	7	US-11-188-298-4162	Sequence 4162, Ap	173	31	51.7	249	6	US-10-793-626-306	Sequence 306, App
101	32	53.3	486	7	US-11-188-298-6889	Sequence 6889, Ap	174	31	51.7	271	6	US-10-506-454-729	Sequence 729, App
102	32	53.3	486	7	US-11-188-298-16022	Sequence 16022, A	175	31	51.7	275	6	US-10-821-234-1013	Sequence 1013, Ap
103	32	53.3	486	7	US-11-188-298-17939	Sequence 17939, A	176	31	51.7	281	7	US-11-096-568A-15342	Sequence 15342, A
104	32	53.3	489	7	US-11-188-298-7248	Sequence 7248, Ap	177	31	51.7	285	5	US-09-978-360A-489	Sequence 489, App
105	32	53.3	491	7	US-11-188-298-4038	Sequence 4038, Ap	178	31	51.7	318	7	US-11-087-099-4152	Sequence 4152, Ap
106	32	53.3	491	7	US-11-188-298-13093	Sequence 13093, A	179	31	51.7	323	7	US-11-079-463-7912	Sequence 7912, Ap
107	32	53.3	494	7	US-11-188-298-12254	Sequence 12254, A	180	31	51.7	333	6	US-10-467-657-316	Sequence 316, App
108	32	53.3	495	7	US-11-188-298-15215	Sequence 15215, A	181	31	51.7	333	6	US-10-467-657-4900	Sequence 4900, Ap
109	32	53.3	499	7	US-11-087-099-11253	Sequence 11253, A	182	31	51.7	334	7	US-11-087-099-9160	Sequence 9160, Ap
110	32	53.3	503	7	US-11-188-298-10771	Sequence 10771, A	183	31	51.7	344	7	US-11-087-099-1929	Sequence 1929, Ap
111	32	53.3	504	7	US-11-188-298-10996	Sequence 10996, A	184	31	51.7	373	6	US-10-498-026-95	Sequence 95, Appl
112	32	53.3	505	7	US-11-188-298-16466	Sequence 16466, A	185	31	51.7	373	6	US-10-498-026-99	Sequence 99, Appl
113	32	53.3	512	7	US-11-087-099-9319	Sequence 9319, Ap	186	31	51.7	374	6	US-10-498-026-96	Sequence 96, Appl
114	32	53.3	519	7	US-11-096-568A-7850	Sequence 7850, Ap	187	31	51.7	374	6	US-10-498-026-100	Sequence 100, App
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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125	37	61.7	661	4	US-10-124-805-552	Sequence 552, App	198	36	60.0	125	4	US-10-219-478-94	Sequence 94, Appl
126	37	61.7	730	4	US-10-087-192-813	Sequence 813, App	199	36	60.0	125	4	US-10-219-524-94	Sequence 94, Appl
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128	37	61.7	743	4	US-10-007-805-494	Sequence 494, App	201	36	60.0	125	4	US-10-216-165-94	Sequence 94, Appl
129	37	61.7	743	4	US-10-076-622-494	Sequence 494, App	202	36	60.0	125	4	US-10-218-956-94	Sequence 94, Appl
130	37	61.7	743	4	US-10-124-805-494	Sequence 494, App	203	36	60.0	125	4	US-10-219-468-94	Sequence 94, Appl
131	37	61.7	826	4	US-10-437-963-133946	Sequence 133946, A	204	36	60.0	125	4	US-10-219-478-94	Sequence 94, Appl
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145	37	61.7	1095	4	US-10-007-805-493	Sequence 493, App	218	36	60.0	125	4	US-10-219-524-94	Sequence 94, Appl
146	37	61.7	1095	4	US-10-076-622-493	Sequence 493, App	219	36	60.0	125	4	US-10-219-528-94	Sequence 94, Appl
147	37	61.7	1095	4	US-10-124-805-493	Sequence 493, App	220	36	60.0	125	4	US-10-227-880-94	Sequence 94, Appl
148	37	61.7	1191	4	US-10-433-577-24	Sequence 24, Appl	221	36	60.0	125	4	US-10-230-436-94	Sequence 94, Appl
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150	37	61.7	1341	4	US-10-076-622-565	Sequence 565, App	223	36	60.0	125	4	US-10-232-223-94	Sequence 94, Appl
151	37	61.7	1341	4	US-10-177-293-334	Sequence 334, App	224	36	60.0	125	4	US-10-232-227-94	Sequence 94, Appl
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153	37	61.7	1341	4	US-10-058-270A-4	Sequence 4, Appl	226	36	60.0	125	4	US-10-232-223-94	Sequence 94, Appl
154	37	61.7	1341	5	US-10-855-588-34	Sequence 34, Appl	227	36	60.0	125	4	US-10-232-223-94	Sequence 94, Appl
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SUMMARIES

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2	60	100.0	32	US-10-091-135-4	Sequence 4, Appli
3	60	100.0	39	US-10-091-135-5	Sequence 5, Appli
4	60	100.0	46	US-10-091-135-6	Sequence 6, Appli
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142	34	56.7	707	1	PCT-US95-11720-18	Sequence 18, Appl	215	33	55.0	1239	1	US-09-285-502-2	Sequence 2, Appli
143	34	56.7	737	2	US-09-583-110-4156	Sequence 4156, Ap	216	33	55.0	1239	2	US-09-709-126-2	Sequence 2, Appli
144	34	56.7	750	1	US-08-325-553-2	Sequence 2, Appli	217	33	55.0	1239	2	US-09-671-385A-2	Sequence 2, Appli
145	34	56.7	750	1	US-08-394-152A-2	Sequence 2, Appli	218	33	55.0	1362	2	US-09-134-001C-4955	Sequence 4955, Ap
146	34	56.7	750	1	US-09-044-668-2	Sequence 2, Appli	219	33	55.0	1442	2	US-09-320-095-2	Sequence 2052, Ap
147	34	56.7	750	2	US-08-705-477E-2	Sequence 4, Appli	220	33	55.0	1442	2	US-09-710-279-2052	Sequence 2, Appli
148	34	56.7	750	2	US-09-973-382C-4	Sequence 4, Appli	221	32	54.2	62	2	US-09-320-095-10	Sequence 10, Appl
149	34	56.7	750	2	US-09-999-833A-618	Sequence 618, App	222	32	54.2	62	2	US-09-320-095-10	Sequence 10, Appl
150	34	56.7	750	2	US-08-466-381C-2	Sequence 2, Appli	223	32	54.2	557	2	US-09-523-487-2	Sequence 60, Appl
151	34	56.7	750	2	US-10-020-445A-618	Sequence 618, App	224	32	54.2	557	2	US-08-488-161-60	Sequence 60, Appl
152	34	56.7	750	2	US-09-561-502-2	Sequence 2, Appli	225	32	53.3	43	1	US-09-273-685-60	Sequence 60, Appl
153	34	56.7	751	2	US-09-107-433-4728	Sequence 4728, Ap	226	32	53.3	43	4	PCT-US95-1193A-60	Sequence 60, Appl
154	34	56.7	769	2	US-09-320-878-12	Sequence 12, Appl	227	32	53.3	65	2	US-09-107-532A-6494	Sequence 6494, Ap
155	34	56.7	769	2	US-09-141-908-10	Sequence 10, Appl	228	32	53.3	130	2	US-09-248-796A-19515	Sequence 19515, A
156	34	56.7	769	2	US-09-657-440-12	Sequence 12, Appl	229	32	53.3	179	2	US-09-605-703B-2850	Sequence 2850, Ap
157	34	56.7	769	2	US-09-783-708-12	Sequence 12, Appl	230	32	53.3	189	2	US-09-800-729-144	Sequence 144, App
158	34	56.7	774	2	US-09-902-540-9843	Sequence 9843, Ap	231	32	53.3	213	2	US-09-270-767-42473	Sequence 42473, A
159	34	56.7	784	2	US-09-740-235-1	Sequence 1, Appli	232	32	53.3	223	2	US-09-949-016-8894	Sequence 8894, Ap
160	34	56.7	809	2	US-09-105-537-24	Sequence 24, Appl	233	32	53.3	267	2	US-09-519-232-68	Sequence 68, Appl
161	34	56.7	1048	2	US-09-171-699-10	Sequence 10, Appl	234	32	53.3	282	2	US-09-252-991A-28272	Sequence 28272, A
162	34	56.7	1165	2	US-09-902-540-12897	Sequence 12897, A	235	32	53.3	313	2	US-09-303-518D-314	Sequence 314, App
163	34	56.7	3782	2	US-09-105-537-4	Sequence 4, Appli	236	32	53.3	313	2	US-09-303-518D-316	Sequence 316, App
164	33	55.0	43	2	US-10-153-185-15	Sequence 15, Appl	237	32	53.3	329	1	US-08-225-477B-3	Sequence 3, Appli
165	33	55.0	44	2	US-10-153-185-2	Sequence 2, Appli	238	32	53.3	329	1	PCT-US95-04353-3	Sequence 3, Appli
166	33	55.0	61	2	US-09-107-532A-5570	Sequence 5570, Ap	239	32	53.3	329	4	PCT-US95-04353-8	Sequence 8, Appli
167	33	55.0	73	2	US-08-248-796A-22754	Sequence 2754, A	240	32	53.3	334	2	US-09-489-039A-13658	Sequence 13658, A
168	33	55.0	260	2	US-09-638-203-3	Sequence 3, Appli	241	32	53.3	337	2	US-09-434-613-1	Sequence 1, Appli
169	33	55.0	275	2	US-09-468-433C-24	Sequence 24, Appl	242	32	53.3	337	2	US-09-963-908-1	Sequence 1, Appli
170	33	55.0	374	2	US-09-489-847-166	Sequence 166, App	243	32	53.3	337	2	US-10-847-165-1	Sequence 1, Appli
171	33	55.0	382	2	US-09-907-794A-137	Sequence 137, App	244	32	53.3	337	2	US-09-716-865-6	Sequence 6, Appli
172	33	55.0	382	2	US-09-905-125A-137	Sequence 137, App	245	32	53.3	486	2	US-09-519-232-16	Sequence 16, Appl
173	33	55.0	382	2	US-09-902-775A-137	Sequence 137, App	246	32	53.3	492	2		

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:24:04 ; Search time 15.3542 Seconds
(without alignments)
59.230 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPCGNKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	204	1	US-08-419-414-9
2	60	100.0	204	1	US-08-614-935-2
3	60	100.0	204	2	US-09-130-287-2
4	60	100.0	227	2	US-09-541-759-6
5	56	93.3	31	1	US-08-614-935-46
6	56	93.3	31	2	US-09-130-287-46
7	54	90.0	204	1	US-08-614-935-1
8	54	90.0	204	2	US-09-130-287-1
9	50	83.3	31	1	US-08-614-935-45
10	50	83.3	31	2	US-09-130-287-45
11	48	80.0	32	1	US-08-614-935-48
12	48	80.0	32	2	US-09-130-287-48
13	48	80.0	205	1	US-08-614-935-4
14	48	80.0	205	2	US-09-130-287-4
15	47	78.3	31	1	US-08-614-935-47
16	47	78.3	31	2	US-09-130-287-47
17	47	78.3	203	1	US-08-419-414-8
18	47	78.3	203	1	US-08-614-935-3
19	47	78.3	203	2	US-09-130-287-3
20	43	71.7	20	1	US-08-614-935-10
21	43	71.7	20	2	US-09-130-287-10
22	43	71.7	32	1	US-08-614-935-49
23	43	71.7	32	2	US-09-130-287-49
24	43	71.7	204	1	US-08-614-935-5
25	43	71.7	204	2	US-09-130-287-5
26	40	66.7	1011	2	US-09-602-362E-27
27	40	66.7	1239	2	US-10-076-622-577

28	39	65.0	20	1	US-08-614-935-9	Sequence 9, Appli
29	39	65.0	20	2	US-09-130-287-9	Sequence 9, Appli
30	39	65.0	32	1	US-08-614-935-42	Sequence 42, Appli
31	39	65.0	32	2	US-09-130-287-42	Sequence 42, Appli
32	39	65.0	705	2	US-09-949-016-10464	Sequence 10464, A
33	37	61.7	409	2	US-09-248-796A-19008	Sequence 19008, A
34	37	61.7	445	2	US-09-620-405B-473	Sequence 473, App
35	37	61.7	445	2	US-09-433-826B-473	Sequence 473, App
36	37	61.7	445	2	US-09-604-287A-473	Sequence 473, App
37	37	61.7	445	2	US-09-834-759-473	Sequence 473, App
38	37	61.7	445	2	US-09-590-751A-473	Sequence 473, App
39	37	61.7	445	2	US-09-551-621-473	Sequence 473, App
40	37	61.7	445	2	US-09-551-621A-473	Sequence 473, App
41	37	61.7	445	2	US-10-076-622-473	Sequence 472, App
42	37	61.7	466	2	US-09-620-405B-472	Sequence 472, App
43	37	61.7	466	2	US-09-433-826B-472	Sequence 472, App
44	37	61.7	466	2	US-09-604-287A-472	Sequence 472, App
45	37	61.7	466	2	US-09-834-759-472	Sequence 472, App
46	37	61.7	466	2	US-09-590-751A-472	Sequence 472, App
47	37	61.7	466	2	US-09-551-621-472	Sequence 472, App
48	37	61.7	466	2	US-09-551-621A-472	Sequence 472, App
49	37	61.7	466	2	US-10-076-622-472	Sequence 472, App
50	37	61.7	650	2	US-09-620-405B-469	Sequence 469, App
51	37	61.7	650	2	US-09-433-826B-469	Sequence 469, App
52	37	61.7	650	2	US-09-604-287A-469	Sequence 469, App
53	37	61.7	650	2	US-09-834-759-469	Sequence 469, App
54	37	61.7	650	2	US-09-590-751A-469	Sequence 469, App
55	37	61.7	650	2	US-09-551-621-469	Sequence 469, App
56	37	61.7	650	2	US-09-551-621A-469	Sequence 469, App
57	37	61.7	650	2	US-10-076-622-469	Sequence 469, App
58	37	61.7	661	2	US-10-076-622-552	Sequence 552, App
59	37	61.7	743	2	US-09-620-405B-494	Sequence 494, App
60	37	61.7	743	2	US-09-834-759-494	Sequence 494, App
61	37	61.7	743	2	US-10-076-622-494	Sequence 494, App
62	37	61.7	829	2	US-09-487-558B-324	Sequence 324, App
63	37	61.7	1002	2	US-09-620-405B-475	Sequence 475, App
64	37	61.7	1002	2	US-09-604-287A-475	Sequence 475, App
65	37	61.7	1002	2	US-09-834-759-475	Sequence 475, App
66	37	61.7	1002	2	US-09-590-751A-475	Sequence 475, App
67	37	61.7	1002	2	US-09-551-621-475	Sequence 475, App
68	37	61.7	1002	2	US-09-551-621A-475	Sequence 475, App
69	37	61.7	1002	2	US-10-076-622-475	Sequence 475, App
70	37	61.7	1013	2	US-10-076-622-553	Sequence 553, App
71	37	61.7	1095	2	US-09-620-405B-493	Sequence 493, App
72	37	61.7	1095	2	US-09-834-759-493	Sequence 493, App
73	37	61.7	1095	2	US-10-076-622-493	Sequence 493, App
74	37	61.7	1341	2	US-09-602-362E-23	Sequence 23, Appli
75	37	61.7	1341	2	US-10-076-622-565	Sequence 565, App
76	37	61.7	1349	2	US-10-076-622-573	Sequence 573, App
77	36	60.0	125	2	US-10-033-301-9	Sequence 9, Appli
78	36	60.0	212	2	US-10-380-105-6	Sequence 6, Appli
79	36	60.0	253	2	US-10-030-808-4	Sequence 4, Appli
80	36	60.0	336	2	US-09-710-279-1858	Sequence 1858, Ap
81	36	60.0	351	2	US-09-134-001C-4387	Sequence 4387, Ap
82	36	60.0	876	2	US-09-949-016-10968	Sequence 10968, A
83	36	60.0	876	2	US-09-949-016-10969	Sequence 10969, A
84	35	58.3	29	2	US-09-346-510B-30	Sequence 30, Appli
85	35	58.3	60	2	US-09-134-000C-4477	Sequence 4477, Ap
86	35	58.3	67	2	US-09-144-838-25	Sequence 25, Appli
87	35	58.3	67	2	US-09-144-838-30	Sequence 30, Appli
88	35	58.3	67	2	US-09-144-838-49	Sequence 49, Appli
89	35	58.3	68	2	US-09-144-838-26	Sequence 26, Appli
90	35	58.3	68	2	US-09-144-838-50	Sequence 50, Appli
91	35	58.3	68	2	US-09-144-838-53	Sequence 53, Appli
92	35	58.3	69	2	US-09-144-838-54	Sequence 54, Appli
93	35	58.3	399	2	US-09-107-532A-4714	Sequence 4714, Ap
94	35	58.3	429	2	US-09-107-532A-3785	Sequence 3785, Ap
95	35	58.3	463	2	US-09-252-991A-27686	Sequence 27686, A
96	35	58.3	1463	2	US-09-583-110-4076	Sequence 4076, Ap
97	35	58.3	1463	2	US-09-107-433-4214	Sequence 4214, Ap
98	34	56.7	83	1	US-07-965-674-2	Sequence 2, Appli
99	34	56.7	83	1	PCT-US93-09523-2	Sequence 2, Appli
100	34	56.7	84	1	US-07-965-674-3	Sequence 3, Appli

105	37	61.7	394	2	Q5APB4 CANAL	Q5apb4 candida alb	178	36	60.0	402	2	Q9AL21_ENTFA	Q9al21 enterococcu
106	37	61.7	406	2	Q9L602_MYCAV	Q9l602 mycobacteri	179	36	60.0	437	2	Q871h0_NEUPA	Q871h0 neurospora
107	37	61.7	414	2	Q6LQ07_PHOPR	Q6lq07 photobacter	180	36	60.0	438	2	Q61ha9_DROME	Q61ha9 drosophila
108	37	61.7	434	2	Q5YA97_9CAUD	Q5ya97 bacillus cl	181	36	60.0	441	2	Q4HX18_GIBZE	Q4hx18 gibberella
109	37	61.7	589	2	Q4L9X3_STAHI	Q4l9x3 staphylococ	182	36	60.0	448	2	Q5B4X6_EMENI	Q5b4x6 aspergillus
110	37	61.7	613	2	Q8TPP0_METAC	Q8tp0 methanosarc	183	36	60.0	459	2	Q45984_CAEEL	Q45984 caenorhabdi
111	37	61.7	623	2	Q83ZD7_STAUA	Q83zd7 staphylococ	184	36	60.0	462	2	Q51N60_MAGGR	Q51n60 magnaporth
112	37	61.7	641	2	Q5IRN0_MOUSE	Q5irn0 mus musculu	185	36	60.0	479	2	Q7NVB1_CHRVO	Q7nvb1 chromobacte
113	37	61.7	653	2	Q5IRN0_MOUSE	Q5irn0 mus musculu	186	36	60.0	481	2	Q7S7L7_NEUCR	Q7s7l7 neurospora
114	37	61.7	653	2	Q8K100_MOUSE	Q8k100 mus musculu	187	36	60.0	494	2	Q4WNT9_ASFPU	Q4wnt9 aspergillus
115	37	61.7	681	2	Q7Q104_ANOGA	Q7q104 anopheles g	188	36	60.0	545	2	Q4UHV6_THEAB	Q4uhv6 thelleria a
116	37	61.7	692	2	Q5US47_9LECA	Q5us47 toxoplasma	189	36	60.0	571	2	Q97DE4_CLOAB	Q97de4 clostridium
117	37	61.7	704	2	Q5US47_9LECA	Q5us47 sarcogyste s	190	36	60.0	576	2	Q92EN3_SYNV3	Q92en3 listeria in
118	37	61.7	710	2	Q9FNC7_ARATH	Q9fnc7 arabidopsis	191	36	60.0	644	2	Q92EN3_SYNV3	Q92en3 synchocyst
119	37	61.7	711	2	Q5US93_9LECA	Q5us93 acarospora	192	36	60.0	653	2	Q41AP6_GIBZE	Q41ap6 gibberella
120	37	61.7	717	2	Q94114_ARATH	Q94114 arabidopsis	193	36	60.0	702	2	Q5ZUH4_CHICK	Q5zuh4 gallus gall
121	37	61.7	741	2	Q6K9F7_ORYSA	Q6k9f7 oryza sativ	194	36	60.0	714	2	Q60149_STRPY	Q60149 streptococ
122	37	61.7	829	2	SIP4_YEAST	P46954 saccharomyc	195	36	60.0	717	2	Q6PST6_SPOPR	Q6pst6 spodoptera
123	37	61.7	968	2	Q7PST6_ANOGA	Q7pst6 anopheles g	196	36	60.0	806	2	Q9VFV0_DROME	Q9vfv0 drosophila
124	37	61.7	1128	2	Q7T5L2_GVCL	Q7t5l2 cryptophleb	197	36	60.0	842	2	Q97DB8_CLOAB	Q97db8 clostridium
125	37	61.7	1131	2	Q91EW5_GVCP	Q91ew5 cydia pomon	198	36	60.0	850	2	Q54R85_DICDI	Q54r85 dictyosteli
126	37	61.7	1234	2	Q64R22_BACPR	Q64r22 bacteroides	199	36	60.0	850	2	Q60182_SCHZO	Q60182 schizosacch
127	37	61.7	1249	2	Q5LAW4_BACFN	Q5law4 bacteroides	200	36	60.0	934	1	Q62021_ORYSA	Q62021 oryza sativ
128	37	61.7	1341	2	Q5W025_HUMAN	Q5w025 homo sapien	201	36	60.0	981	2	Q54R85_DICDI	Q54r85 dictyosteli
129	37	61.7	1341	2	Q9BXX3_HUMAN	Q9bxx3 homo sapien	202	36	60.0	1048	1	Q62021_ORYSA	Q62021 oryza sativ
130	37	61.7	1460	2	Q5W026_HUMAN	Q5w026 homo sapien	203	36	60.0	1234	2	Q81A6Z2_BACTN	Q81a6z2 bacteroides
131	37	61.7	1882	2	Q857A5_9CAUD	Q857a5 mycobacteri	204	36	60.0	1285	2	Q7S2A3_ASHGO	Q7s2a3 ashaya goss
132	37	61.7	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila	205	36	60.0	1306	2	Q5NXC4_MOUSE	Q5nxc4 mus musculu
133	37	61.7	3843	2	Q9VU94_DROME	Q9vu94 drosophila	206	36	60.0	1390	2	Q51UE4_MAGGR	Q51ue4 magnaporth
134	36	60.0	66	1	RS27_SULSO	Q9vz80 sulfolobus	207	36	60.0	1422	2	Q692A2_MOUSE	Q692a2 mus musculu
135	36	60.0	73	1	RS27_AERPE	Q9yfol aeropyrum p	208	36	60.0	1514	2	Q9H0B0_HUMAN	Q9h0b0 homo sapien
136	36	60.0	82	2	Q5BS94_SCHJA	Q5bs94 schistosoma	209	36	60.0	1563	2	Q5NXC5_MOUSE	Q5nxc5 mus musculu
137	36	60.0	92	2	Q69JEB_ORYSA	Q69jeb oryza sativ	210	36	60.0	1564	2	Q96JN8_HUMAN	Q96jn8 homo sapien
138	36	60.0	96	2	Q9ZTJ4_MAIZE	Q9ztj4 zea mays (m	211	36	60.0	1792	2	Q4Z244_PLABE	Q4z244 plasmodium
139	36	60.0	100	2	Q73OM9_TREDE	Q73om9 treponema d	212	35	58.3	55	2	Q8XP03_CLOPE	Q8xp03 clostridium
140	36	60.0	106	2	Q8CR22_STAEP	Q8cr22 staphylococ	213	35	58.3	58	2	Q56BP3_9CAUD	Q56bp3 enterobacte
141	36	60.0	120	2	Q6WLR4_LEGPN	Q6wlr4 legionella	214	35	58.3	55	2	Q8B671_9HIV1	Q8b671 human immun
142	36	60.0	120	2	Q5L5Y4_ENTHI	Q5l5y4 entamoeba h	215	35	58.3	70	2	Q84F10_CLOPE	Q84f10 clostridium
143	36	60.0	122	2	Q6UXB1_HUMAN	Q6uxb1 homo sapien	216	35	58.3	72	2	Q46251_CLOPE	Q46251 clostridium
144	36	60.0	125	2	Q50T97_ENTHI	Q50t97 entamoeba h	217	35	58.3	76	2	Q9SP92_MESMA	Q9sp92 mesobuthus
145	36	60.0	171	2	Q50T97_ENTHI	Q50t97 entamoeba h	218	35	58.3	82	2	Q8XQR3_RALSO	Q8xqr3 ralstonia s
146	36	60.0	180	1	S3DR_CLOAB	Q97j95 clostridium	219	35	58.3	89	2	Q5PEW8_SALPA	Q5pew8 salmonella
147	36	60.0	180	2	Q6MMK8_BACCE	Q6mmk8 bacillus ce	220	35	58.3	90	2	Q5WYF7_LEGPL	Q5wyf7 legionella
148	36	60.0	180	2	Q6HFA5_BACHK	Q6hfa5 bacillus th	221	35	58.3	91	2	Q6K6H2_ORYSA	Q6k6h2 oryza sativ
149	36	60.0	180	2	Q732V6_BACC1	Q732v6 bacillus ce	222	35	58.3	98	2	Q5X705_LEGPA	Q5x705 legionella
150	36	60.0	180	2	Q81A24_BACCR	Q81a24 bacillus ce	223	35	58.3	98	2	Q5X705_LEGPA	Q5x705 legionella
151	36	60.0	180	2	Q63606_BACC2	Q63606 bacillus ce	224	35	58.3	105	2	Q58622_PYRHO	Q58622 pyrococcus
152	36	60.0	180	2	Q81WR2_BACAN	Q81wr2 bacillus an	225	35	58.3	109	1	Q58622_PYRHO	Q58622 pyrococcus
153	36	60.0	189	2	Q87KD9_VIBPA	Q87kd9 vibrio para	226	35	58.3	115	2	Q8XZB8_RALSO	Q8xzb8 ralstonia s
154	36	60.0	192	2	Q4L9F5_STAHI	Q4l9f5 staphylococ	227	35	58.3	118	2	Q15902_TOXGO	Q15902 toxoplasma
155	36	60.0	214	2	Q624G4_CAEER	Q624g4 caenorhabdi	228	35	58.3	126	2	Q4YZ80_PLABE	Q4yz80 plasmodium
156	36	60.0	221	2	Q6APG7_DESPS	Q6apg7 desulfotale	229	35	58.3	129	1	Y2370_ARCFU	Y2370 archaeoglob
157	36	60.0	235	2	Q5ZS37_LEGPH	Q5zs37 legionella	230	35	58.3	151	2	Q8LNC2_ORYSA	Q8lnc2 oryza sativ
158	36	60.0	238	2	Q4P2T8_USTMA	Q4p2t8 ustilago ma	231	35	58.3	153	2	Q6K785_ORYSA	Q6k785 oryza sativ
159	36	60.0	244	2	Q49533_ARATH	Q49533 arabidopsis	232	35	58.3	162	2	Q96VN5_SULTO	Q96vn5 sulfolobus
160	36	60.0	252	2	Q94JD6_ORYSA	Q94jd6 oryza sativ	233	35	58.3	163	2	Q77P34_9CAUD	Q77p34 lactococcus
161	36	60.0	253	1	LEP4_VIBCH	P27717 vibrio chol	234	35	58.3	164	2	Q94MA2_9CAUD	Q94ma2 lactococcus
162	36	60.0	253	2	Q7BG59_VIBCH	Q7bg59 vibrio chol	235	35	58.3	164	2	Q62Y89_BACLD	Q62y89 bacillus ll
163	36	60.0	254	2	Q5BBS2_EMENI	Q5bbs2 aspergillus	236	35	58.3	165	2	Q65MU5_BACLD	Q65mu5 bacillus ll
164	36	60.0	282	2	Q5V690_HALMA	Q5v690 haloarcula	237	35	58.3	172	2	Q92TJ5_MAIZE	Q92tj5 zea mays (m
165	36	60.0	292	2	Q6SR59_WANSM	Q6sr59 manniemia	238	35	58.3	178	2	Q5CXU3_CRYPV	Q5cxu3 cryptospori
166	36	60.0	315	2	Q43888_STRAQ	Q43888 streptococ	239	35	58.3	189	2	Q5CIT2_CRYVO	Q5cit2 cryptospori
167	36	60.0	336	2	Q5HL38_STAEO	Q5hl38 staphylococ	240	35	58.3	189	2	Q8DD99_VIBVU	Q8dd99 vibrio vuln
168	36	60.0	340	2	Q8BLT4_MOUSE	Q8blt4 mus musculu	241	35	58.3	202	2	Q8B620_VIBVU	Q8b620 vibrio vuln
169	36	60.0	356	2	Q6AAN6_PROAC	Q6aan6 propionibac	242	35	58.3	203	1	HOP2_YEAST	HOP2 yeast
170	36	60.0	357	2	Q4L307_STAHI	Q4l307 staphylococ	243	35	58.3	209	2	Q9A0Q2_STRPY	Q9a0q2 streptococ
171	36	60.0	359	2	Q9HL10_THEAC	Q9hl10 thermoplas	244	35	58.3	214	2	Q5XYL2_BORGA	Q5xyl2 borrelia ga
172	36	60.0	361	1	SERC_YEREN	P19689 yersinia en	245	35	58.3	215	2	Q4HE74_DESVH	Q4he74 campylobact
173	36	60.0	361	1	SERC_YERPE	Q8zgb4 yersinia pe	246	35	58.3	224	2	Q72F26_DESVH	Q72f26 desulfovibr
174	36	60.0	361	1	SERC_YERPS	Q66ci9 yersinia ps	247	35	58.3	231	2	Q7MGL0_VIBVY	Q7mg10 vibrio vuln
175	36	60.0	366	2	Q4P4F6_USTMA	Q4p4t6 ustilago ma	248	35	58.3	235	2	Q93VI9_ARATH	Q93vi9 arabidopsis
176	36	60.0	376	2	Q4F7D0_USTMA	Q4f7d0 ustilago ma	249	35	58.3	280	1	VPS71_YEAST	VPS71 yeast
177	36	60.0	385	2	Q4NGAB_9MICC	Q4ngab arthrobacte	250	35	58.3				

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Run on: April 18, 2006, 11:16:43 ; Search time 115.958 Seconds

(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPCNGNKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	204	1 VA5_VESFL	P35783 vespula fla
2	60	100.0	227	1 VA5_VESVU	Q05110 vespula vul
3	59	98.3	204	1 VA5_VESPE	P35785 vespula pen
4	54	90.0	204	1 VA5_VESMC	P35760 vespula mac
5	48	80.0	204	1 VA5_VESGE	P35784 vespula ger
6	47	78.3	203	1 VA5_DOLAR	Q05108 dolichovesp
7	46	76.7	205	1 VA5_VESSQ	P35786 vespula squ
8	46	76.7	215	1 VA53_DOLMA	P10737 dolichovesp
9	45	75.0	886	2 Q9LYI8_ARATH	Q91y18 arabidopsis
10	44	73.3	172	2 Q8FSZ5_METWA	Q8p325 methanogarc
11	44	73.3	694	2 Q9GZ15_DROME	Q9g215 drosophila
12	44	73.3	783	2 Q7KUY7_DROME	Q7kuy7 drosophila
13	44	73.3	840	2 Q9VKL1_DROME	Q9vkl1 drosophila
14	43	71.7	55	2 Q9HKN0_TREAC	Q9hkn0 thermoplas
15	43	71.7	227	1 VA52_DOLMA	P10736 dolichovesp
16	41	68.3	202	1 VA51_VESCR	P35781 vespa crabr
17	41	68.3	202	1 VA52_VESCR	P35782 vespa crabr
18	41	68.3	202	1 VA5_VESMA	P81657 vespa manda
19	41	68.3	203	2 P97777_RAT	P97777 rattus norv
20	41	68.3	411	2 Q7PSB6_ANOGA	Q7psb6 anopheles g
21	41	68.3	467	1 ADECL1_MOUSE	Q9rx02 mus musculu
22	41	68.3	717	2 Q6S156_ASF	Q6s156 african swi
23	40	66.7	63	2 Q37667_9HIV1	Q37667 human immun
24	40	66.7	184	2 Q5YFD4_9VIRU	Q5yfd4 singapore g
25	40	66.7	201	2 Q6MU65_MYCWS	Q6mu65 mycoplasma
26	40	66.7	206	1 VA5_VESV1	P35787 vespula vid
27	40	66.7	216	2 P90053_9HIV1	P90053 human immun
28	40	66.7	274	2 Q5V6C3_HALMA	Q5v6c3 haloarcula
29	40	66.7	443	2 Q4WDW9_ASPFU	Q4wdw9 aspergillus
30	40	66.7	454	2 Q4L8L4_STAHL	Q4l8l4 staphylococ
31	40	66.7	472	2 Q9W2Y4_DROME	Q9w2y4 drosophila

32	40	66.7	496	2 Q8GHV4_PSERE	Q8ghv4 pseudomonas
33	40	66.7	720	2 Q8XIY0_CLOPE	Q8xiy0 clostridium
34	40	66.7	791	2 Q4I5I6_GIBZE	Q4i5i6 gibberella
35	40	66.7	796	2 Q8A5U3_BACTN	Q8a5u3 bacteroides
36	40	66.7	798	2 Q64PL2_BACFR	Q64pl2 bacteroides
37	40	66.7	864	2 Q4UEY4_THEAN	Q4uey4 theileria a
38	40	66.7	882	2 Q5L9C8_BACFN	Q5l9c8 bacteroides
39	40	66.7	1011	2 Q9BXK2_HUMAN	Q9bxk2 homo sapien
40	40	66.7	1196	2 Q8BG77_PARTE	Q8bg77 paramecium
41	40	66.7	3133	2 Q54FD2_DICDI	Q54fd2 dictyosteli
42	39.5	65.8	1312	2 Q6BIP6_DBHHA	Q6bip6 debaryomyce
43	39	65.0	60	2 Q7U5L7_RHOBA	Q7u5l7 rhodospirell
44	39	65.0	146	2 Q9LYV7_ARATH	Q9lyv7 arabidopsis
45	39	65.0	235	2 Q5WTB6_LRGPL	Q5wtb6 legionella
46	39	65.0	235	2 Q5X1K7_LEGPA	Q5x1k7 legionella
47	39	65.0	245	2 Q7LD91_DROYA	Q7ld91 drosophila
48	39	65.0	247	2 Q9X1S9_THEMEA	Q9x1s9 thermocoga
49	39	65.0	323	2 Q5OV00_ENTHI	Q5ov00 entamoeba h
50	39	65.0	344	2 Q6TVK6_9POXV	Q6tvk6 orf virus.
51	39	65.0	346	2 Q6TVV6_9POXV	Q6tvv6 orf virus.
52	39	65.0	351	2 Q9UX43_SULSO	Q9ux43 sulfolobus
53	39	65.0	437	2 Q54C11_DICDI	Q54cd1 dictyosteli
54	39	65.0	460	1 SYG_STRAC	Q82br9 streptomyce
55	39	65.0	460	1 SYG_PROAC	Q912h9 streptomyce
56	39	65.0	472	1 SYG_PROAC	Q86gd7 crassostrea
57	39	65.0	599	2 Q86GD7_CRAGI	Q86gd7 crassostrea
58	39	65.0	627	2 Q6U9G1_9CAUD	Q6u9g1 bacterioph
59	39	65.0	627	2 Q56EM2_9CAUD	Q56em2 aeromonas p
60	39	65.0	819	1 ADAM9_HUMAN	Q13443 homo sapien
61	39	65.0	845	1 ADAM9_MOUSE	Q61072 mus musculu
62	39	65.0	845	2 Q58GH6_RAT	Q58gh6 rattus norv
63	39	65.0	2072	2 Q7RSW8_PLAYO	Q7rsw8 plasmodium
64	38	63.3	72	2 Q4V110_BACCC	Q4v110 bacillus ce
65	38	63.3	116	2 Q4WJD3_ASPFU	Q4wjd3 aspergillus
66	38	63.3	182	2 Q65JE3_BACLD	Q65je3 bacillus li
67	38	63.3	295	2 Q9HEH0_NEUCR	Q9heh0 neurospora
68	38	63.3	323	2 Q34789_BACSU	Q34789 bacillus su
69	38	63.3	324	2 Q65MY2_BACLD	Q65my2 bacillus li
70	38	63.3	356	1 Y1773_VIBCH	Q9kr70 vibrio chol
71	38	63.3	376	2 Q7FVP3_ANOGA	Q7fvp3 anopheles g
72	38	63.3	384	2 Q51IL2_MAGGR	Q51il2 magnaporthe
73	38	63.3	385	2 Q972Z1_SULTO	Q972z1 sulfolobus
74	38	63.3	391	2 Q7FVP2_ANOGA	Q7fvp2 anopheles g
75	38	63.3	469	2 Q5N3X4_STNP6	Q5n3x4 synecococc
76	38	63.3	697	2 Q9VU11_DROME	Q9vu11 drosophila
77	38	63.3	823	2 Q6LYN4_METMP	Q6lyn4 methanococ
78	38	63.3	1169	2 Q6ZQH3_MOUSE	Q6zqh3 mus musculu
79	38	63.3	1622	2 Q5R888_PONPY	Q5r888 pongo pygma
80	38	63.3	1753	2 Q7LE74_MOUSE	Q7le74 mus musculu
81	38	63.3	2067	1 NCOA6_MOUSE	Q9j119 m nuclear r
82	38	63.3	2069	2 Q5XJV5_MOUSE	Q5xjv5 mus musculu
83	38	63.3	2151	2 Q9NG79_TRIVA	Q9ng79 trichomonas
84	38	63.3	2511	2 Q81L44_PLAF7	Q81l44 plasmodium
85	38	63.3	2623	2 Q54SZ1_DICDI	Q54sz1 dictyosteli
86	38	63.3	4483	2 Q51QB7_MAGGR	Q51qb7 magnaporthe
87	37	61.7	66	1 RS27_SULTO	Q973f9 sulfolobus
88	37	61.7	67	2 Q7VNL5_HAEDU	Q7vnl5 haemophilus
89	37	61.7	115	2 Q9M5V2_SOYBN	Q9m5v2 glycine max
90	37	61.7	126	2 Q5TG92_HUMAN	Q5tg92 homo sapien
91	37	61.7	134	2 Q94CDA_ARATH	Q94cd4 arabidopsis
92	37	61.7	149	2 Q725D6_LISMF	Q725d6 listeria mo
93	37	61.7	156	2 Q20386_CABEL	Q20386 clostridum
94	37	61.7	175	2 Q899U7_CLOTE	Q899u7 clostridum
95	37	61.7	181	1 COTE_BACSU	Q038u7 ctenorhabdi
96	37	61.7	182	2 Q5L0E6_GROKA	Q5l0e6 geobacillus
97	37	61.7	206	2 Q9K4H7_STRCO	Q9k4h7 streptomyce
98	37	61.7	208	2 Q4Q3Q5_AZOVI	Q4q3q5 azotobacter
99	37	61.7	295	1 Y8145_PYRPU	Q8u1r0 pyrococcus
100	37	61.7	295	1 Y8145_PYRPU	Q9v0d9 pyrococcus
101	37	61.7	295	1 Y949_PYRHO	Q58667 pyrococcus
102	37	61.7	347	2 Q5FIM6_LACAC	Q5fim6 lactobacill
103	37	61.7	369	2 Q6ZB86_ORYSA	Q6zb86 oryza sativ
104	37	61.7	386	2 Q50723_BORBU	Q50729 borrella bu

103	34	56.7	616	2	A99969	anaerobic ribonuc	176	33	55.0	1231	2	T18550	reverse gyrase cha
104	34	56.7	641	2	AD1724	NADH oxidase homol	177	33	55.0	1239	2	T13809	probable disintegr
105	34	56.7	735	2	E95023	anaerobic ribonuc	178	32.5	54.2	66	2	H70077	hypothetical prote
106	34	56.7	737	2	G97894	ribonucleoside-tri	179	32	53.3	106	2	E71618	hypothetical prote
107	34	56.7	750	2	A56881	prostate-specific	180	32	53.3	111	2	F56556	zinc-ribon transcri
108	34	56.7	765	2	G96896	protein FLN21.14 [181	32	53.3	124	2	T26799	fork head homolog
109	34	56.7	787	2	C84898	hypothetical prote	182	32	53.3	121	2	T40344	hypothetical prote
110	34	56.7	835	2	T05259	probable disease r	183	32	53.3	128	2	F43363	hypothetical zinc
111	34	56.7	878	2	F64425	valine-tRNA ligase	184	32	53.3	130	2	AF1908	hypothetical prote
112	34	56.7	1048	1	XPB2A9	large structural p	185	32	53.3	153	2	AI0772	probable exported
113	34	56.7	1056	2	T00060	hypothetical prote	186	32	53.3	159	2	JQ0542	185K secretory pro
114	34	56.7	1369	2	S58160	hypothetical prote	187	32	53.3	160	2	AF1908	serine O-acetyltra
115	34	56.7	1503	2	T43166	alpha-2-macroglobu	188	32	53.3	171	1	B64671	o-serine acetyltra
116	34	56.7	2212	2	A41098	calcium channel pr	189	32	53.3	171	2	B71845	hypothetical prote
117	34	56.7	3759	2	A35085	trithorax protein	190	32	53.3	181	2	E36794	GTP-binding protei
118	34	56.7	3828	2	T13857	trithorax protein	191	32	53.3	215	2	F34323	hypothetical prote
119	33.5	55.8	602	2	T47794	hypothetical prote	192	32	53.3	215	2	A30413	hypothetical prote
120	33	55.0	55	2	F82858	hypothetical prote	193	32	53.3	221	2	F84431	hypothetical prote
121	33	55.0	57	2	G64372	hypothetical prote	194	32	53.3	221	2	F45067	hypothetical prote
122	33	55.0	61	2	A64392	hypothetical prote	195	32	53.3	236	2	T51276	hypothetical prote
123	33	55.0	114	2	S70116	hypothetical prote	196	32	53.3	245	2	F64347	hypothetical prote
124	33	55.0	123	2	AC2234	hypothetical prote	197	32	53.3	259	2	E71975	conserved hypotet
125	33	55.0	138	2	G40605	response regulator	198	32	53.3	260	2	S27422	peroxisomal assem
126	33	55.0	146	2	B84180	hypothetical prote	199	32	53.3	271	2	S27422	hypothetical prote
127	33	55.0	157	2	T28321	ORF MSV160 hypote	200	32	53.3	294	2	G90032	hypothetical prote
128	33	55.0	158	2	D90391	conserved hypotet	201	32	53.3	305	2	S29711	oligofactory factor
129	33	55.0	161	2	F71117	hypothetical prote	202	32	53.3	313	2	G81782	adhesin MafA2 NMA2
130	33	55.0	211	2	T48794	hypothetical prote	203	32	53.3	313	2	G81782	adhesin mafa - Nel
131	33	55.0	230	2	T26896	mem protein - phag	204	32	53.3	314	1	G64658	probable pyruvate
132	33	55.0	241	1	ZQBPMQ	hypothetical prote	205	32	53.3	314	1	A71858	pyruvate ferredoxi
133	33	55.0	250	2	AB0421	PNP protein (limp)	206	32	53.3	330	2	G90256	DNA primase, proba
134	33	55.0	279	2	T16014	hypothetical prote	207	32	53.3	347	2	D96590	hypothetical prote
135	33	55.0	332	1	A55897	prolactin-induced	208	32	53.3	362	1	E64187	phosphoserine tran
136	33	55.0	342	1	G70460	conserved hypotet	209	32	53.3	365	2	E90099	hypothetical prote
137	33	55.0	370	2	A72572	hypothetical prote	210	32	53.3	370	2	S29139	aggreccan - pig (fr
138	33	55.0	402	2	D70186	xylose operon regu	211	32	53.3	374	2	E83894	hypothetical prote
139	33	55.0	404	2	C81274	hypothetical prote	212	32	53.3	375	2	E85035	hypothetical prote
140	33	55.0	409	2	S55178	probable sphingoli	213	32	53.3	377	2	T06643	zinc metalloprotei
141	33	55.0	464	2	S50592	hypothetical prote	214	32	53.3	387	2	T19370	hypothetical prote
142	33	55.0	470	2	T16606	probable serine ca	215	32	53.3	397	2	H72668	hypothetical prote
143	33	55.0	474	1	IMBP4	site-specific reco	216	32	53.3	405	2	F81273	hypothetical prote
144	33	55.0	500	1	S02302	aldehyde dehydroge	217	32	53.3	415	2	C82168	hypothetical prote
145	33	55.0	501	1	DEHUE1	aldehyde dehydroge	218	32	53.3	425	2	T48993	hypothetical prote
146	33	55.0	501	1	JQ1004	aldehyde dehydroge	219	32	53.3	428	2	T39773	adenylosuccinate s
147	33	55.0	501	2	S14752	aldehyde dehydroge	220	32	53.3	433	1	S48515	hypothetical prote
148	33	55.0	501	2	JC4534	aldehyde dehydroge	221	32	53.3	465	2	C84083	hypothetical prote
149	33	55.0	501	2	JC5553	aldehyde dehydroge	222	32	53.3	471	2	T26612	hypothetical prote
150	33	55.0	540	2	A71630	aldehyde dehydroge	223	32	53.3	474	2	T27006	G-protein signalin
151	33	55.0	544	2	S26425	HSP60 fold T-compl	224	32	53.3	481	2	S62427	2-hydroxymuconic s
152	33	55.0	569	2	H87926	site-specific DNA-	225	32	53.3	486	2	S10772	hypothetical prote
153	33	55.0	594	2	T23841	protein ClpD12.7 [226	32	53.3	491	2	H84840	actin bundling pro
154	33	55.0	600	2	T49281	hypothetical prote	227	32	53.3	493	2	I38621	aldehyde dehydroge
155	33	55.0	610	2	T23836	fertilin alpha pre	228	32	53.3	501	1	A32616	4-carboxy-2-hydrox
156	33	55.0	630	2	D97992	hypothetical prote	229	32	53.3	505	2	T31272	hypothetical prote
157	33	55.0	641	2	AC1354	hypothetical prote	230	32	53.3	506	2	S58150	aldehyde dehydroge
158	33	55.0	657	2	T48228	NADH oxidase homol	231	32	53.3	509	1	S14629	hypothetical prote
159	33	55.0	660	2	A28153	probable protein k	232	32	53.3	518	2	E84536	hypothetical prote
160	33	55.0	662	2	S70365	gelatinase A (EC 3	233	32	53.3	525	2	T20662	hypothetical prote
161	33	55.0	662	2	A42436	gelatinase A (EC 3	234	32	53.3	535	2	T32139	hypothetical prote
162	33	55.0	662	2	S34780	gelatinase A (EC 3	235	32	53.3	543	2	I40545	oligopeptide ABC t
163	33	55.0	663	1	S46492	gelatinase A (EC 3	236	32	53.3	546	2	T40258	probable t-complex
164	33	55.0	669	2	T16636	hypothetical prote	237	32	53.3	557	2	T43202	probable chaperoni
165	33	55.0	709	2	E64213	DNA topoisomerase	238	32	53.3	572	2	T40856	probable nucleotid
166	33	55.0	718	1	A69084	SHE4 protein - yea	239	32	53.3	616	1	RRVQLL	probable RNA-direc
167	33	55.0	789	2	S62172	exoribonuclease RN	240	32	53.3	638	1	RRVQWA	conserved hypotet
168	33	55.0	793	2	AI1380	exoribonuclease RN	241	32	53.3	638	2	T44763	beta-N-acetylhexos
169	33	55.0	793	2	AB1750	probable permease	242	32	53.3	639	2	AC3895	beta-N-acetylhexos
170	33	55.0	832	2	G97146	hypothetical prote	243	32	53.3	657	2	F97670	hypothetical prote
171	33	55.0	977	2	S62540	DNA-directed DNA p	244	32	53.3	663	1	E69475	DNA topoisomerase
172	33	55.0	1092	2	H69071	reverse gyrase - A	245	32	53.3	663	2	C97120	topoisomerase I [1
173	33	55.0	1146	2	B70376	hypothetical prote	246	32	53.3	697	2	C97120	transforming prote
174	33	55.0	1156	2	T23748	hypothetical prote	247	32	53.3	751	1	I49497	
175	33	55.0	1207	2	T23754	hypothetical prote	248	32	53.3	751	1	I49497	

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 18.3333 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPNCGNKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	204	A44583	venom allergen ant
2	59	98.3	204	C44583	venom allergen ant
3	54	90.0	204	B37329	antigen 5 - easter
4	48	80.0	204	B44583	venom allergen ant
5	48	80.0	213	B31085	antigen 5-3 precu
6	46	76.7	205	D44583	venom allergen ant
7	45	75.0	886	T48544	MAP3K delta-1 prot
8	43	71.7	227	A31085	antigen 5-2 precu
9	41	68.3	202	H44583	venom allergen ant
10	41	68.3	202	G44583	venom allergen ant
11	40	66.7	206	E44583	venom allergen ant
12	39	65.0	146	T48566	hypothetical prote
13	39	65.0	247	E72233	conserved hypotet
14	39	65.0	351	G90212	conserved hypotet
15	39	65.0	655	JC7850	disintegrin and me
16	39	65.0	660	S71949	metalloproteinase
17	38	63.3	323	E69789	hypothetical prote
18	38	63.3	356	B82159	conserved hypotet
19	37	61.7	142	T22156	hypothetical prote
20	37	61.7	181	A31245	outer spore coat p
21	37	61.7	295	D75131	mrp-family probabl
22	37	61.7	295	H71085	probable MRP prote
23	37	61.7	386	F70231	conserved hypotet
24	37	61.7	653	I48341	endoglin - mouse
25	37	61.7	829	S50246	SIP4 protein - yea
26	36	60.0	66	B90257	SSU ribosomal prot
27	36	60.0	73	G72737	probable ribosomal
28	36	60.0	180	C97050	phage related prote
29	36	60.0	244	T01761	hypothetical prote

30	36	60.0	253	1	A40582	type IV prelin p
31	36	60.0	253	2	D82273	leader peptidase T
32	36	60.0	315	2	I39479	hypothetical prote
33	36	60.0	361	1	XNEBPY	phosphoserine tran
34	36	60.0	361	2	AG0169	phosphoserine tran
35	36	60.0	459	2	T27657	hypothetical prote
36	36	60.0	571	2	H97333	site-specific modi
37	36	60.0	576	2	S75958	hypothetical prote
38	36	60.0	644	2	AB1486	transcription anti
39	36	60.0	714	2	S68603	hypothetical prote
40	36	60.0	842	2	B97337	ABC-type transport
41	36	60.0	891	2	T19915	hypothetical prote
42	36	60.0	934	2	T39941	hypothetical prote
43	35	58.3	105	2	B71081	hypothetical prote
44	35	58.3	109	2	T38145	DNA-directed RNA p
45	35	58.3	116	2	I84704	gene VII048 protei
46	35	58.3	201	2	B69546	conserved hypotet
47	35	58.3	202	2	T05763	hypothetical prote
48	35	58.3	280	2	S52479	hypothetical prote
49	35	58.3	323	2	T01626	peroxidase (EC 1.1
50	35	58.3	329	2	T14077	peroxidase (EC 1.1
51	35	58.3	329	2	T04710	peroxidase (EC 1.1
52	35	58.3	329	2	T04709	peroxidase (EC 1.1
53	35	58.3	357	2	A86825	hypothetical prote
54	35	58.3	384	2	C82159	conserved hypotet
55	35	58.3	484	2	G86362	beta-glucanase (im
56	35	58.3	679	2	S64258	hypothetical prote
57	35	58.3	1312	2	T32758	hypothetical prote
58	35	58.3	1463	2	C95032	DNA-directed DNA p
59	35	58.3	1463	2	C97903	voltage-gated sodi
60	35	58.3	1695	2	JE0084	aggrean precursor
61	35	58.3	2109	1	I50421	arietin - puff add
62	34	56.7	30	2	S15982	hypothetical prote
63	34	56.7	50	2	B82816	hypothetical prote
64	34	56.7	81	2	A34899	bitan alpha - puff
65	34	56.7	83	2	F35982	hypothetical prote
66	34	56.7	84	2	S42603	hypothetical prote
67	34	56.7	85	2	AB2872	conserved hypotet
68	34	56.7	85	2	E97648	hypothetical prote
69	34	56.7	109	2	F90242	conserved hypotet
70	34	56.7	188	2	T51271	hypothetical prote
71	34	56.7	210	2	T45903	hypothetical prote
72	34	56.7	254	2	F69547	nucleotide-binding
73	34	56.7	254	2	A95216	type II restrictio
74	34	56.7	254	2	A31975	endonuclease dpnc
75	34	56.7	254	2	G98079	type II site-speci
76	34	56.7	256	2	G96692	hypothetical prote
77	34	56.7	258	2	T32542	hypothetical prote
78	34	56.7	266	2	C72380	hypothetical prote
79	34	56.7	294	2	S73232	ribosomal protein
80	34	56.7	317	2	S76723	hypothetical prote
81	34	56.7	322	2	D86228	hypothetical prote
82	34	56.7	324	2	T46213	hypothetical prote
83	34	56.7	331	2	C72339	hypothetical prote
84	34	56.7	350	2	A64813	ybhH protein - Eac
85	34	56.7	350	2	F85579	hypothetical prote
86	34	56.7	350	2	E90728	hypothetical prote
87	34	56.7	359	2	D96910	muconate cyclisom
88	34	56.7	365	2	A30800	conserved hypotet
89	34	56.7	365	2	F98206	hypothetical 37.1K
90	34	56.7	389	1	SYPUF	hypothetical prote
91	34	56.7	391	2	T14580	naevigin-chalcon
92	34	56.7	406	2	AC2007	SIP4 protein pre
93	34	56.7	406	2	A12497	transposase allr60
94	34	56.7	411	2	B91220	transposase allr716
95	34	56.7	411	2	D86066	probable arylsulfa
96	34	56.7	411	2	A65184	probable arylsulfa
97	34	56.7	448	2	T29040	arylsulfatase aci
98	34	56.7	473	2	I49283	hypothetical prote
99	34	56.7	473	2	A86442	ADAM 4 protein pre
100	34	56.7	493	2	T12304	hypothetical prote
101	34	56.7	583	2	A85588	catalase (EC 1.1.1
102	34	56.7	583	2	H90737	hypothetical prote

98	37	61.7	185	4	AAB63933	Aab63933 Human pro	171	37	61.7	3843	4	ABB71529	Abb71529 Drosophila
99	37	61.7	189	4	AAB63929	Aab63929 Human pro	172	36	60.0	62	4	AM20362	Aam20362 Peptide #
100	37	61.7	195	4	AAB63918	Aab63918 Human pro	173	36	60.0	62	4	AB40953	Ab40953 Peptide #
101	37	61.7	207	4	AAB63937	Aab63937 Human pro	174	36	60.0	62	4	AB34727	Ab34727 Peptide #
102	37	61.7	220	4	AAB63917	Aab63917 Human pro	175	36	60.0	62	4	AB25065	Ab25065 Protein #
103	37	61.7	223	4	AAB63903	Aab63903 Human pro	176	36	60.0	62	4	AM74616	Aam74616 Human bon
104	37	61.7	225	4	AAB63901	Aab63901 Human pro	177	36	60.0	62	4	AM61815	Aam61815 Human bon
105	37	61.7	229	4	AAB63925	Aab63925 Human pro	178	36	60.0	62	4	AB56400	Ab56400 Human liv
106	37	61.7	241	7	ADB83983	Aab63925 Human pro	179	36	60.0	62	4	AB56400	Ab56400 Human liv
107	37	61.7	266	4	AAB63899	Aab63899 Human pro	180	36	60.0	102	5	AB56400	Ab56400 Human liv
108	37	61.7	295	4	AAB63899	Aab63899 Human pro	181	36	60.0	125	2	AB56400	Ab56400 Human liv
109	37	61.7	343	8	ADY1828	Ady1828 Putative	182	36	60.0	125	3	AB56400	Ab56400 Human liv
110	37	61.7	390	8	ADY1828	Ady1828 Putative	183	36	60.0	125	3	AB56400	Ab56400 Human liv
111	37	61.7	394	5	ABP73544	Abp73544 Candida a	184	36	60.0	125	4	AB56400	Ab56400 Human liv
112	37	61.7	398	3	ABP73544	Abp73544 Candida a	185	36	60.0	125	4	AB56400	Ab56400 Human liv
113	37	61.7	445	4	AAB50249	Aab50249 Human bre	186	36	60.0	125	5	AB56400	Ab56400 Human liv
114	37	61.7	445	4	AAB50249	Aab50249 Human bre	187	36	60.0	125	5	AB56400	Ab56400 Human liv
115	37	61.7	445	4	AAB50249	Aab50249 Human bre	188	36	60.0	125	5	AB56400	Ab56400 Human liv
116	37	61.7	445	5	ABG78917	Aab50249 Human bre	189	36	60.0	125	5	AB56400	Ab56400 Human liv
117	37	61.7	445	6	ABJ37740	Abj37740 Human tum	190	36	60.0	125	5	AB56400	Ab56400 Human liv
118	37	61.7	445	7	ADL93135	Adl93135 Human bre	191	36	60.0	125	5	AB56400	Ab56400 Human liv
119	37	61.7	445	8	ADL93135	Adl93135 Human bre	192	36	60.0	125	5	AB56400	Ab56400 Human liv
120	37	61.7	466	4	AAB50248	Aab50248 Human bre	193	36	60.0	125	6	AB56400	Ab56400 Human liv
121	37	61.7	466	4	AAB50248	Aab50248 Human bre	194	36	60.0	125	6	AB56400	Ab56400 Human liv
122	37	61.7	466	4	AAB50248	Aab50248 Human bre	195	36	60.0	125	6	AB56400	Ab56400 Human liv
123	37	61.7	466	5	ABG78916	Abg78916 Human bre	196	36	60.0	125	6	AB56400	Ab56400 Human liv
124	37	61.7	466	6	ABJ37739	Abj37739 Human tum	197	36	60.0	125	6	AB56400	Ab56400 Human liv
125	37	61.7	466	7	ADL93134	Adl93134 Human bre	198	36	60.0	125	6	AB56400	Ab56400 Human liv
126	37	61.7	466	8	ADL93134	Adl93134 Human bre	199	36	60.0	125	6	AB56400	Ab56400 Human liv
127	37	61.7	466	8	ADL93134	Adl93134 Human bre	200	36	60.0	125	6	AB56400	Ab56400 Human liv
128	37	61.7	650	4	AAB50263	Aab50263 Human bre	201	36	60.0	125	6	AB56400	Ab56400 Human liv
129	37	61.7	650	4	AAB50263	Aab50263 Human bre	202	36	60.0	125	6	AB56400	Ab56400 Human liv
130	37	61.7	650	5	AAB50263	Aab50263 Human bre	203	36	60.0	125	6	AB56400	Ab56400 Human liv
131	37	61.7	650	6	ABJ37736	Abj37736 Human tum	204	36	60.0	125	6	AB56400	Ab56400 Human liv
132	37	61.7	650	7	ADL93131	Adl93131 Human bre	205	36	60.0	125	6	AB56400	Ab56400 Human liv
133	37	61.7	650	8	ADL93131	Adl93131 Human bre	206	36	60.0	125	6	AB56400	Ab56400 Human liv
134	37	61.7	653	5	ADL93131	Adl93131 Human bre	207	36	60.0	125	7	AB56400	Ab56400 Human liv
135	37	61.7	661	6	ABJ37782	Abj37782 Human tum	208	36	60.0	125	7	AB56400	Ab56400 Human liv
136	37	61.7	661	7	ADL93214	Adl93214 Human bre	209	36	60.0	125	7	AB56400	Ab56400 Human liv
137	37	61.7	730	7	ABM85466	Abm85466 Mouse pro	210	36	60.0	125	7	AB56400	Ab56400 Human liv
138	37	61.7	733	4	AAB50263	Aab50263 Human bre	211	36	60.0	125	7	AB56400	Ab56400 Human liv
139	37	61.7	743	5	ABG78925	Abg78925 Human bre	212	36	60.0	125	7	AB56400	Ab56400 Human liv
140	37	61.7	743	6	ABJ37748	Abj37748 Human tum	213	36	60.0	125	7	AB56400	Ab56400 Human liv
141	37	61.7	743	7	ADL93156	Adl93156 Human bre	214	36	60.0	125	7	AB56400	Ab56400 Human liv
142	37	61.7	829	5	ABP35670	Abp35670 Fungal 2B	215	36	60.0	125	7	AB56400	Ab56400 Human liv
143	37	61.7	829	8	ADT87129	Adt87129 Yeast Str	216	36	60.0	125	7	AB56400	Ab56400 Human liv
144	37	61.7	1002	4	AAB50263	Aab50263 Human bre	217	36	60.0	125	7	AB56400	Ab56400 Human liv
145	37	61.7	1002	5	ABG78918	Abg78918 Human bre	218	36	60.0	125	7	AB56400	Ab56400 Human liv
146	37	61.7	1002	6	ABJ37741	Abj37741 Human tum	219	36	60.0	125	7	AB56400	Ab56400 Human liv
147	37	61.7	1002	7	ADL93137	Adl93137 Human bre	220	36	60.0	125	7	AB56400	Ab56400 Human liv
148	37	61.7	1002	8	ADL93137	Adl93137 Human bre	221	36	60.0	125	7	AB56400	Ab56400 Human liv
149	37	61.7	1013	6	ABJ37783	Abj37783 Human tum	222	36	60.0	125	7	AB56400	Ab56400 Human liv
150	37	61.7	1013	7	ADL93215	Adl93215 Human bre	223	36	60.0	125	7	AB56400	Ab56400 Human liv
151	37	61.7	1030	6	ABU20850	Abu20850 Protein e	224	36	60.0	125	7	AB56400	Ab56400 Human liv
152	37	61.7	1095	4	AAB50263	Aab50263 Human bre	225	36	60.0	125	7	AB56400	Ab56400 Human liv
153	37	61.7	1095	5	ABG78924	Abg78924 Human bre	226	36	60.0	125	7	AB56400	Ab56400 Human liv
154	37	61.7	1095	6	ABJ37747	Abj37747 Human tum	227	36	60.0	125	7	AB56400	Ab56400 Human liv
155	37	61.7	1095	7	ADL93155	Adl93155 Human bre	228	36	60.0	125	7	AB56400	Ab56400 Human liv
156	37	61.7	1191	5	AAB50263	Aab50263 Human bre	229	36	60.0	125	7	AB56400	Ab56400 Human liv
157	37	61.7	1339	9	ABA20113	Aba20113 Novel hum	230	36	60.0	125	7	AB56400	Ab56400 Human liv
158	37	61.7	1341	4	AAB84702	Aab84702 Amino aci	231	36	60.0	125	7	AB56400	Ab56400 Human liv
159	37	61.7	1341	5	ABJ05537	Abj05537 Breast ca	232	36	60.0	125	7	AB56400	Ab56400 Human liv
160	37	61.7	1341	6	ABJ37784	Abj37784 Human tum	233	36	60.0	125	7	AB56400	Ab56400 Human liv
161	37	61.7	1341	7	ABR47548	Abra47548 Breast ca	234	36	60.0	125	7	AB56400	Ab56400 Human liv
162	37	61.7	1341	8	ADL93227	Adl93227 Human bre	235	36	60.0	125	7	AB56400	Ab56400 Human liv
163	37	61.7	1341	9	ADT49017	Adt49017 Human BFA	236	36	60.0	125	7	AB56400	Ab56400 Human liv
164	37	61.7	1341	10	ADU99254	Adu99254 BFA5 tumo	237	36	60.0	125	7	AB56400	Ab56400 Human liv
165	37	61.7	1341	11	ADV60459	Adv60459 Human bre	238	36	60.0	125	7	AB56400	Ab56400 Human liv
166	37	61.7	1341	12	ADY93219	Ady93219 Human NY-	239	36	60.0	125	8	AB56400	Ab56400 Human liv
167	37	61.7	1349	6	ABJ37788	Abj37788 Human tum	240	36	60.0	125	8	AB56400	Ab56400 Human liv
168	37	61.7	1349	7	ADL93235	Adl93235 Human bre	241	36	60.0	125	8	AB56400	Ab56400 Human liv
169	37	61.7	1397	9	ADY93228	Ady93228 Human NY-	242	36	60.0	125	8	AB56400	Ab56400 Human liv
170	37	61.7	1432	6	ABU24715	Abu24715 Protein e	243	36	60.0	125	8	AB56400	Ab56400 Human liv

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 96.7083 Seconds
(without alignments)
49.977 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPCNGKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

A_Geneseq_21:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	11	5	Aae28815 Vespula v
2	60	100.0	32	5	Aae28810 Vespula v
3	60	100.0	39	5	Aae28811 Vespula v
4	60	100.0	46	5	Aae28812 Vespula v
5	60	100.0	50	5	Aae28827 Vespula v
6	60	100.0	57	5	Aae28828 Vespula v
7	60	100.0	76	5	Aae28829 Vespula v
8	60	100.0	204	2	Aay45217 Wild type
9	60	100.0	204	2	Aay45217 Wild type
10	60	100.0	204	5	ABG66983 Wasp veno
11	60	100.0	204	5	ABG67052 Wasp veno
12	60	100.0	204	5	ABG67104 Wasp veno
13	60	100.0	204	5	ABG67103 Wasp veno
14	60	100.0	204	5	Aae28820 Vespula v
15	60	100.0	209	4	Abm00031 Allergen
16	60	100.0	227	2	Aay25644 Vespula s
17	60	100.0	227	4	Aae13071 Vespula v
18	60	100.0	227	2	Adc34893 Wasp alle
19	56	93.3	31	2	Aaw35648 T cell pe
20	54	90.0	204	2	Aaw35687 Wasp veno
21	54	90.0	204	5	ABG66977 Wasp veno
22	54	83.3	31	2	Aaw35647 T cell pe
23	48	80.0	32	2	Aaw35650 T cell pe
24	48	80.0	205	2	Aaw35690 Vespid an

QY 1 HYTMVWANTKEVCGSGSIKVEKWHKHYLVNCGPSGNFKNEELYQTK 49
DB 158 HYTMVWANTKEVCGSGSVKVDWETHYLVNCGPSGNFKNEELYQTK 206

US-10-986-405-197
; Sequence 197, Application US/10986405
; Publication No. US20060073561A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: 157 Human Secreted Proteins
; FILE REFERENCE: P2750P1
; CURRENT APPLICATION NUMBER: US/10/986,405
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: PCT/US2003/015439
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/388,543
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/401,757
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US 60/381,592
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/402,585
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 60/404,959
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/415,902
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/402,799
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 378
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-986-405-197
Query Match 43.2%; Score 123; DB 6; Length 270;
Best Local Similarity 49.0%; Pred. No. 1.5e-08;
Matches 25; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 HYTMVWANTKEVCGSGSIKVEKWHKHYLVNCGPSGNFKNEELYQTK 47
DB 128 HYTMVWANTKEVCGSGSHFCEKLGVEETNIELLVNCGYPPGNVKGKRPYQ 178

US-11-272-833-4
; Sequence 4, Application US/11272833
; Publication No. US20060063924A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Ruben, Steven M.
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Leukocyte Regulatory Factors 1 and 2
; FILE REFERENCE: P2359
; CURRENT APPLICATION NUMBER: US/11/272,833
; CURRENT FILING DATE: 2005-11-15
; PRIOR APPLICATION NUMBER: US/05/055,998
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/043,483
; PRIOR FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-272-833-4

Query Match 43.2%; Score 123; DB 7; Length 443;
Best Local Similarity 49.0%; Pred. No. 2.4e-08;
Matches 25; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 HYTMVWANTKEVCGSGSIKVEKWHKHYLVNCGPSGNFKNEELYQTK 47
DB 128 HYTMVWANTKEVCGSGSHFCEKLGVEETNIELLVNCGYPPGNVKGKRPYQ 178

US-10-131-826A-360
; Sequence 360, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarsoff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 360
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-360

Query Match 43.2%; Score 123; DB 6; Length 463;
Best Local Similarity 49.0%; Pred. No. 2.5e-08;
Matches 25; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 12.1565 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYTMWANTKEVCGSGSIKY.....LVCNYGPGNFKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New: *
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2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
7: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	97.9	227	6	US-10-498-026-76
2	237	83.2	206	6	US-10-498-026-80
3	123	43.2	270	6	US-10-986-405-197
4	123	43.2	443	7	US-11-272-833-4
5	123	43.2	463	6	US-10-131-826A-360
6	123	43.2	463	6	US-10-973-115B-360
7	123	43.2	463	7	US-11-154-673-9
8	123	43.2	463	7	US-11-290-153-360
9	123	43.2	506	7	US-11-154-673-2
10	123	43.2	550	7	US-11-154-673-8
11	123	43.2	593	7	US-11-154-673-3
12	123	43.2	625	7	US-11-154-673-7
13	116	40.7	258	7	US-11-090-439-38
14	111.5	39.1	245	6	US-10-515-868-6
15	111	38.9	383	6	US-10-453-372-88
16	111	38.9	457	6	US-10-453-372-84
17	111	38.9	475	6	US-10-453-372-98
18	111	38.9	477	6	US-10-453-372-90
19	111	38.9	497	6	US-10-453-372-92
20	111	38.9	497	6	US-10-453-372-100
21	111	38.9	497	6	US-10-453-372-102
22	111	38.9	497	6	US-10-218-784-56
23	111	38.9	497	6	US-10-219-061-56
24	111	38.9	497	6	US-10-219-062-56
25	111	38.9	497	6	US-10-219-064-56

26	111	38.9	497	6	US-10-233-134-56	Sequence 56, Appl
27	111	38.9	498	6	US-10-453-372-94	Sequence 94, Appl
28	109	38.2	243	6	US-10-515-868-4	Sequence 4, Appl
29	109	38.2	243	6	US-10-506-443A-41	Sequence 41, Appl
30	108.5	38.1	242	6	US-10-131-826A-262	Sequence 262, App
31	108.5	38.1	242	6	US-10-973-115B-262	Sequence 262, App
32	108.5	38.1	242	7	US-11-290-153-262	Sequence 262, App
33	106	37.2	500	6	US-10-194-487-70	Sequence 70, Appl
34	106	37.2	500	6	US-10-195-883-70	Sequence 70, Appl
35	106	37.2	500	6	US-10-195-888-70	Sequence 70, Appl
36	106	37.2	500	6	US-10-195-889-70	Sequence 70, Appl
37	106	37.2	500	7	US-11-067-573-2	Sequence 2, Appl
38	99.5	34.9	190	7	US-11-031-206-90	Sequence 90, Appl
39	98.5	34.6	216	7	US-11-038-285A-9	Sequence 9, Appl
40	98.5	34.6	219	7	US-11-272-833-7	Sequence 7, Appl
41	98.5	34.6	220	7	US-11-153-222A-3	Sequence 3, Appl
42	98.5	34.6	221	7	US-11-038-285A-11	Sequence 11, Appl
43	98.5	34.6	231	7	US-11-038-285A-10	Sequence 10, Appl
44	98.5	34.6	265	7	US-11-038-285A-7	Sequence 7, Appl
45	98.5	34.6	266	7	US-11-038-285A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76

Query Match 97.9%; Score 279; DB 6; Length 227;
Best Local Similarity 98.0%; Pred. No. 5.8e-29;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYTMWANTKEVCGSGSIKYIQEKWHKHYLCVNYGPGNFKNEELYQTK 49
Db 179 HYTMWANTKEVCGSGSIKYIQEKWHKHYLCVNYGPGNFKNEELYQTK 227

RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80

Query Match 83.2%; Score 237; DB 6; Length 206;
Best Local Similarity 73.5%; Pred. No. 1.6e-23;
Matches 36; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

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; ORGANISM: Vespula vulgaris
US-10-091-135-16

Query Match      100.0%; Score 285; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
|||||
Db 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
|||||

RESULT 3
US-10-719-553-39
; Sequence 39, Application US/10719553
; Publication No. US20040091500A1
; GENERAL INFORMATION:
; APPLICANT: Ipsen, Hans Henrik
; APPLICANT: Spangfort, Michael Dho
; APPLICANT: Larsen Jorgen Nedergaard
; TITLE OF INVENTION: NOVEL RECOMBINANT ALLERGENS
; FILE REFERENCE: 04305/100E144-US2
; CURRENT APPLICATION NUMBER: US/10/719,553
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 09/270,910
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/078,371
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 204
; TYPE: PRT
; ORGANISM: vespula vulgaris
US-10-719-553-39

Query Match      100.0%; Score 285; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
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Db 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 4
US-09-957-806A-22
; Sequence 22, Application US/09957806A
; Publication No. US20050181446A1
; GENERAL INFORMATION:
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; APPLICANT: Svendsen, Allan
; APPLICANT: Friis, Esben
; APPLICANT: Osten, Claus
; TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
; FILE REFERENCE: 10021.204-US
; CURRENT APPLICATION NUMBER: US/09/957,806A
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-09-957-806A-22

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Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
|||||
Db 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
|||||

us-10-091-135-8.rapbm

; ORGANISM: Vespula vulgaris
US-10-091-135-16

Query Match      100.0%; Score 285; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
|||||
Db 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 5
US-10-001-245-214
; Sequence 214, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Vespula vulgaris
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(210)
; OTHER INFORMATION: where X is any amino acid
US-10-001-245-214

Query Match      100.0%; Score 285; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
|||||
Db 162 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 210
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RESULT 6
US-10-091-135-64
; Sequence 64, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-091-135-64

Query Match      97.9%; Score 279; DB 4; Length 204;
Best Local Similarity 98.0%; Pred. No. 6.3e-28;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
|||||
Db 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 7
US-10-091-135-64
; Sequence 64, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-091-135-64

Query Match      97.9%; Score 279; DB 4; Length 204;
Best Local Similarity 98.0%; Pred. No. 6.3e-28;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
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Db 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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2	285	100.0	204	4	US-10-091-135-16	Sequence 16, Appl	
3	285	100.0	204	4	US-10-091-135-39	Sequence 39, Appl	
4	285	100.0	209	3	US-09-557-806A-22	Sequence 22, Appl	
5	285	100.0	210	4	US-10-001-245-214	Sequence 214, App	
6	279	97.9	204	4	US-10-091-135-64	Sequence 64, Appl	
7	279	97.9	204	4	US-10-091-135-81	Sequence 81, Appl	
8	279	97.9	227	3	US-09-847-208-170	Sequence 170, App	
9	279	97.9	227	5	US-10-809-689-82	Sequence 82, Appl	
10	277	97.2	204	3	US-09-847-208-162	Sequence 62, App	
11	277	97.2	204	4	US-10-091-135-65	Sequence 65, Appl	
12	276	96.8	204	3	US-09-847-208-165	Sequence 165, App	
13	276	96.8	204	4	US-10-091-135-63	Sequence 63, Appl	
14	275	96.5	204	3	US-09-847-208-163	Sequence 163, App	
15	275	96.5	204	4	US-10-091-135-67	Sequence 67, Appl	
16	271	95.1	203	4	US-10-001-245-118	Sequence 118, App	
17	268	94.0	204	3	US-09-847-208-166	Sequence 166, App	
18	268	94.0	204	4	US-10-091-135-66	Sequence 66, Appl	
19	255.5	89.6	198	4	US-10-001-245-121	Sequence 121, App	
20	255.5	89.6	202	4	US-10-001-245-117	Sequence 117, App	
21	251.5	88.2	201	4	US-10-001-245-119	Sequence 119, App	
22	249.5	87.5	192	4	US-10-001-245-122	Sequence 122, App	
23	240	84.2	184	4	US-10-001-245-120	Sequence 120, App	
24	237	83.2	206	3	US-09-847-208-171	Sequence 171, App	
25	237	83.2	206	4	US-10-091-135-68	Sequence 68, Appl	
26	237	83.2	206	5	US-10-809-689-86	Sequence 86, Appl	
27	227	79.6	202	3	US-09-847-208-172	Sequence 172, App	

QY 1 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 49
156 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 204
Db

RESULT 2
US-08-614-935-2
; Sequence 2, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
US-08-614-935-2
Query Match 97.9%; Score 279; DB 1; Length 204;
Best Local Similarity 98.0%; Pred. No. 7.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 49
156 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 3
US-09-130-287-2
; Sequence 2, Application US/09130287
; Patent No. 6106844
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,287
; FILING DATE: 2000-04-03
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
US-09-130-287-2
Query Match 97.9%; Score 279; DB 2; Length 204;
Best Local Similarity 98.0%; Pred. No. 7.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 49
156 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 204
Db

RESULT 4
US-09-541-759-6
; Sequence 6, Application US/09541759
; Patent No. 6723322
; GENERAL INFORMATION:
; APPLICANT: Lustigman, Sara
; APPLICANT: Pearlmann, Eric
; APPLICANT: Unnasch, Thomas
; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
; FILE REFERENCE: 63475/252
; CURRENT APPLICATION NUMBER: US/09/541,759
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 6
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vesputula vulgaris
US-09-541-759-6
Query Match 97.9%; Score 279; DB 2; Length 227;
Best Local Similarity 98.0%; Pred. No. 8.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 14.7748 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYTQWVWANTKEVGGSIKY.....LVCNYGPGSNFKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/ECTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	97.9	204	1	US-08-419-414-9
2	279	97.9	204	1	US-08-614-935-2
3	279	97.9	204	2	US-09-130-287-2
4	279	97.9	227	2	US-09-541-759-6
5	276	96.8	204	1	US-08-614-935-1
6	276	96.8	204	2	US-09-130-287-1
7	226	79.3	203	1	US-08-419-414-8
8	226	79.3	203	1	US-08-614-935-3
9	226	79.3	203	2	US-09-130-287-3
10	217	76.1	205	1	US-08-614-935-4
11	217	76.1	205	2	US-09-130-287-4
12	210	73.7	166	1	US-08-614-935-30
13	210	73.7	166	2	US-09-130-287-30
14	210	73.7	204	1	US-08-614-935-5
15	210	73.7	204	2	US-09-130-287-5
16	203	71.2	125	1	US-07-857-224B-114
17	196	68.8	124	1	US-07-857-224B-113
18	189	66.3	205	1	US-08-614-935-7
19	189	66.3	205	2	US-09-130-287-7
20	181	63.5	205	1	US-08-419-414-10
21	181	63.5	205	1	US-08-614-935-6
22	181	63.5	205	2	US-09-130-287-6
23	123	43.2	20	1	US-08-614-935-76
24	123	43.2	20	2	US-09-130-287-76
25	123	43.2	270	1	US-08-773-368-1
26	123	43.2	270	2	US-09-199-887-1
27	123	43.2	463	2	US-09-907-794A-285

28	123	43.2	463	2	US-09-905-125A-285	Sequence 285, App
29	123	43.2	463	2	US-09-902-775A-285	Sequence 285, App
30	123	43.2	463	2	US-09-906-700A-285	Sequence 285, App
31	123	43.2	463	2	US-09-903-603A-285	Sequence 285, App
32	123	43.2	463	2	US-09-904-920A-285	Sequence 285, App
33	123	43.2	463	2	US-09-909-064A-285	Sequence 285, App
34	123	43.2	463	2	US-09-905-361A-285	Sequence 285, App
35	123	43.2	463	2	US-09-906-618-285	Sequence 285, App
36	123	43.2	463	2	US-09-906-646-285	Sequence 285, App
37	123	43.2	463	2	US-09-904-462-285	Sequence 285, App
38	123	43.2	463	2	US-09-902-736A-285	Sequence 285, App
39	123	43.2	463	2	US-09-906-722A-285	Sequence 285, App
40	118	41.4	20	1	US-08-614-935-75	Sequence 75, Appl
41	118	41.4	20	2	US-09-130-287-75	Sequence 75, Appl
42	111.5	39.1	167	1	US-08-773-368-5	Sequence 5, Appl
43	111.5	39.1	167	2	US-09-199-887-5	Sequence 3, Appl
44	111.5	39.1	258	2	US-09-698-781-3	Sequence 112, App
45	109	38.2	138	1	US-07-857-224B-112	

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30109-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
; US-08-419-414-9

Query Match 97.9%; Score 279; DB 1; Length 204;
Best Local Similarity 98.0%; Pred. No. 7.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FT DISULFID 31 By similarity.
 FT DISULFID 49 By similarity.
 FT DISULFID 193 By similarity.
 FT CONFLICT 109 V -> I (in Ref. 2).
 FT CONFLICT 118 Q -> E (in Ref. 2).
 FT CONFLICT 173 D -> N (in Ref. 2).
 FT CONFLICT 219 M -> K (in Ref. 2).
 FT HELIX 26
 FT HELIX 32
 FT TURN 33
 FT TURN 38
 FT HELIX 41
 FT STRAND 53
 FT HELIX 61
 FT TURN 80
 FT TURN 87
 FT TURN 88
 FT STRAND 94
 FT STRAND 101
 FT HELIX 104
 FT TURN 115
 FT STRAND 133
 FT HELIX 141
 FT HELIX 149
 FT HELIX 158
 FT TURN 165
 FT HELIX 169
 FT HELIX 174
 FT TURN 184
 FT TURN 186
 FT TURN 190
 FT STRAND 201
 FT TURN 203
 FT STRAND 219
 FT TURN 220
 FT STRAND 226
 FT STRAND 227
 SQ SEQUENCE 227 AA; 99E9813740A66F55 CRC64;

Query Match 97.9%; Score 279; DB 1; Length 227;
 Best Local Similarity 98.0%; Pred. No. 1.3e-27;
 Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTMWANTKEVCGSGIKYIQEKWHKHYLVNCGSPGNFQNEELYQTK 49
 |||||
 DB 179 HYTMWANTKEVCGSGIKYIQEKWHKHYLVNCGSPGNFQNEELYQTK 227
 |||||

RESULT 2
 VA5 VESFL
 ID VA5 VESFL STANDARD; PRT; 204 AA.
 AC P35783; 1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves f 5) (Ves f V).
 OS Vesputia flavopilosa (Yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespula.
 OX NCBI_TaxID=30211;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94044316; PubMed=8227862;
 RA Hoffman D.R.;
 RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity".
 RL J. Allergy Clin. Immunol. 92:707-716(1993).
 CC -/- FUNCTION: May have an ancestral function in the promotion of ovum fertilization by sperm.
 CC -/- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -/- ALLERGEN: Causes an allergic reaction in human.
 CC -/- SIMILARITY: Belongs to the CRISP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not removed.
 CC PIR; A44583; A44583.
 CC HSSP; Q05110; IQNX.
 DR SMR; P35783; 1-204.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR InterPro; IPR002413; V5_allergen.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; CRISP_1; 1.
 DR PROSITE; PS01010; CRISP_2; 1.
 DR Allergen; Direct protein sequencing.
 FT DISULFID 4 17 By similarity.
 FT DISULFID 8 101 By similarity.
 FT DISULFID 26 94 By similarity.
 FT DISULFID 170 187 By similarity.
 SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;

Query Match 97.2%; Score 277; DB 1; Length 204;
 Best Local Similarity 95.9%; Pred. No. 2.1e-27;
 Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMWANTKEVCGSGIKYIQEKWHKHYLVNCGSPGNFQNEELYQTK 49
 |||||
 DB 156 HYTMWANTKEVCGSGIKYIQEKWHKHYLVNCGSPGNFQNEELYQTK 204
 |||||

RESULT 3
 VA5 VESMC
 ID VA5 VESMC STANDARD; PRT; 204 AA.
 AC P35760;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves m 5) (Ves m V).
 OS Vesputia maculifrons (Eastern yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespula.
 OX NCBI_TaxID=7453;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=93203603; PubMed=8454859;
 RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
 RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets".
 RL J. Immunol. 150:2823-2830(1993).
 CC -/- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -/- ALLERGEN: Causes an allergic reaction in human.
 CC -/- SIMILARITY: Belongs to the CRISP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC PIR; B37329; B37329.
 CC HSSP; Q05110; IQNX.
 DR SMR; P35760; 1-204.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR InterPro; IPR002413; V5_allergen.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; CRISP_1; 1.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 72.3779 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYQMWANTKEVCGSIKY.....LVCNYGSPGNKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	97.9	227	1	VA5_VESVU Q05110 vespula vul
2	277	97.2	204	1	VA5_VESFL P35783 vespula fla
3	276	96.8	204	1	VA5_VESMC P35760 vespula mac
4	275	96.5	204	1	VA5_VESGE P35784 vespula ger
5	268	94.0	204	1	VA5_VESPE P35785 vespula pen
6	237	83.2	206	1	VA5_VESVI P35787 vespula vid
7	227	79.6	202	1	VA5_VESMA P81657 vespula manda
8	226	79.3	202	1	VA51_VESCR P35781 vespula crabr
9	226	79.3	203	1	VA5_DOLAR Q05108 dolichovesp
10	225	78.9	205	1	VA5_VESSQ P35786 vespula equ
11	217	76.1	215	1	VA53_DOLMA P10737 dolichovesp
12	215	75.4	202	1	VA52_VESCR P35782 vespula crabr
13	210	73.7	227	1	VA52_DOLMA P10736 dolichovesp
14	195	68.4	206	1	VA5_POLD0 P81656 polistes do
15	195	68.4	227	2	Q58KJ8_POLD0 P81656 polistes do
16	194	68.1	207	1	VA5_POLGA P83377 polistes ga
17	194	68.1	207	1	VA5_POLSR Q72156 polystia scu
18	189	66.3	205	1	VA5_POLEX P35779 solenopsis ex
19	187	65.6	211	1	VA3_SOLRI P35779 solenopsis ex
20	182.5	64.0	226	2	Q58KJ9_POLEX P35780 polistes ex
21	182	63.9	205	1	VA5_POLFU Q05109 polistes fu
22	181	63.5	209	1	VA5_POLAN P35778 solenopsis an
23	164.5	57.7	234	1	VA3_SOLIN Q58D34 bos taurus
24	132	46.3	464	2	Q7YS25 rhodnius pr
25	129.5	45.4	250	2	O7YS25 RHOPR Q8CHU4 mus musculu
26	127	44.6	474	2	Q8CHU4_MOUSE Q9ET66 mus musculu
27	127	44.6	489	2	Q9ET66_MOUSE Q9JJ56 mus musculu
28	127	44.6	489	2	Q9JJ56_MOUSE Q6ZV9V homo sapien
29	123	43.2	270	2	Q6ZV9V_HUMAN Q8TCB8 homo sapien
30	123	43.2	408	2	Q8TCB8_HUMAN Q8IYL8 homo sapien
31	123	43.2	428	2	Q8IYL8_HUMAN

RESULT 1

VA5_VESVU

ID VA5_VESVU STANDARD; PRT; 227 AA.

AC Q05110; Q9UB91;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Venom allergen 5 precursor (Antigen 5) (Ags) (Allergen Ves v 5) (Ves v V).

DE Vespula vulgaris (Yellow jacket) (Wasps).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespula.

OX NCBI_TaxID=7454;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=93203603; PubMed=8454859;

RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;

RT "Sequence analysis and antigenic cross-reactivity of a venom allergen,

RT antigen 5, from hornets, wasps, and yellow jackets.";

RL J. Immunol. 150:2823-2830(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE OF 24-227.

RA Suck R., Hagen S., Fiebig H.;

RT "Molecular cloning of a genomic sequence from the venom allergen

RT antigen 5 from Vespula vulgaris.";

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoir.

CC -!- ALLERGEN: Causes an allergic reaction in human.

CC -!- SIMILARITY: Belongs to the CRISP family.

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CC EMBL; M98858; AAA30333.1; -; mRNA.

DR EMBL; AJ238849; CAB42887.1; -; Genomic_DNA.

DR PDB; 1ONX; X-ray; A=24-227.

DR InterPro; IPR001283; Allrgn_V5/Tpx1.

DR InterPro; IPR002413; V5_allergen.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00838; VSALLERGEN.

DR PRINTS; PR00837; VSTPXLKE.

DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; CRISP 1; 1.

DR PROSITE; PS01010; CRISP 2; 1.

KW 3D-structure; Allergen; Direct protein sequencing; Signal.

FT SIGNAL 1 23

FT CHAIN 24 227 Venom allergen 5.

FT DISULFID 27 40 By similarity.

32	123	43.2	463	2	Q6UXB8_HUMAN	Q6uxb8 homo sapien
33	123	43.2	463	2	Q8NBK0_HUMAN	Q8nbk0 homo sapien
34	122.5	43.0	363	2	Q5DA03_SCHJA	Q5da03 schistosoma
35	122	42.8	881	1	PRY3_YEAST	P47033 saccharomyc
36	121	42.5	210	2	Q7Z1H1_NECAM	Q7z1h1 necator ame
37	120	42.1	188	2	Q9Z0U6_RAT	Q9z0u6 rattus norv
38	120	42.1	246	2	Q60ZV8_CAEHR	Q60zv8 caenorhabdi
39	120	42.1	246	2	P90958_CAEEL	P90958 caenorhabdi
40	120	42.1	429	2	Q614N2_CAEHR	Q614n2 caenorhabdi
41	119	41.8	494	2	Q9D2R3_MOUSE	Q9d2r3 mus musculu
42	119	41.8	495	2	Q8BZQ2_MOUSE	Q8bzq2 mus musculu
43	118	41.4	253	2	Q9H3Y0_HUMAN	Q9h3y0 homo sapien
44	118	41.4	504	2	Q69HL7_CIOIN	Q69hl7 ciona intes
45	116	40.7	258	2	Q43692_HUMAN	Q43692 homo sapien

ALIGNMENTS

Df 158 HYTQMVAKTKEIGCGSVKYKDEWYHYLVNCYNGPSGNFRNEKLYEKK 202
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
RESULT 6
G44583
venom allergen antigen Vesp c 5.01 - European hornet
C/Species: Vespa crabro (European hornet)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-
C/Accession: G44583; G44522
R/Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A>Title: Allergens in hymenoptera venom XXV: the amino acid sequenc
A/Reference number: A44583; MUID:94044316; PMID:8227862
A/Acession: G44583
A>Status: preliminary
A/Molecule type: protein
A/Residues: 1-202 <HOF>
A/Cross-references: UNIPROT:P35781; UNIPARC:UIP000013807C
C/Superfamily: yellowjacket venom allergen antigen 5

Query Match 79.3%; Score 226; DB 2; Length 202;
Best Local Similarity 73.5%; Pred.No.7e+21;
Matches 36; Conservative 6; Mismatches 7; Indels 0;

Qy 1 HYTQMVAWTKEVCGGSIKIQTCKWKHKHYLVNCYNGPSGNFKNEELYQTK 49
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 154 HYTQMVAKTKEIGCGSIKIENGMRHRHYLVNCYNGPGAGNVEPIYERK 202

RESULT 7
D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C/Species: Vespula squamosa (southern yellowjacket)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-
C/Acession: D44583; D44522
R/Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A>Title: Allergens in hymenoptera venom XXV: the amino acid sequenc
A/Reference number: A44583; MUID:94044316; PMID:8227862
A/Acession: D44583
A>Status: preliminary
A/Molecule type: protein
A/Residues: 1-205 <HOF>
A/Cross-references: UNIPROT:P35786; UNIPARC:UIP0000138094
C/Superfamily: yellowjacket venom allergen antigen 5

Query Match 78.9%; Score 225; DB 2; Length 205;
Best Local Similarity 71.4%; Pred.No.9.5e+21;
Matches 35; Conservative 7; Mismatches 7; Indels 0;

Qy 1 HYTQMVAWTKEVCGGSIKIQTCKWKHKHYLVNCYNGPSGNFKNEELYQTK 49
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 157 HYTQMVAKTKEIGCGSIKYVDNNWYHYLVNCYNGPGAGNFQGVEYVERK 205

RESULT 8
H44583
venom allergen antigen Vesp c 5.02 - European hornet
C/Species: Vespa crabro (European hornet)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-
C/Acession: H44583; H44522
R/Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A>Title: Allergens in hymenoptera venom XXV: the amino acid sequenc
A/Reference number: A44583; MUID:94044316; PMID:8227862
A/Acession: H44583
A>Status: preliminary
A/Molecule type: protein
A/Residues: 1-202 <HOF>
A/Cross-references: UNIPROT:P35782; UNIPARC:UIP0000138080
C/Superfamily: yellowjacket venom allergen antigen 5

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 10.2863 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYTQWVWANTKEVGGSGIKY.....LVNCYGPGSNFKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	97.2	204	2 A44583	venom allergen ant
2	276	96.8	204	2 B37329	antigen 5 - easter
3	275	96.5	204	2 B44583	venom allergen ant
4	268	94.0	204	2 C44583	venom allergen ant
5	237	83.2	206	2 E44583	venom allergen ant
6	226	79.3	202	2 G44583	venom allergen ant
7	225	78.9	205	2 D44583	venom allergen ant
8	215	75.4	202	2 H44583	venom allergen ant
9	213	74.7	213	2 B31085	antigen 5-3 precu
10	210	73.7	227	2 A31085	antigen 5-2 precu
11	189	66.3	205	2 A37329	antigen 5 - paper
12	187	65.6	211	2 B58853	venom allergen Sol
13	182	63.9	205	2 F44583	venom allergen ant
14	159.5	56.0	212	2 B37330	venom allergen III
15	122	42.8	881	2 S56032	probable membrane
16	120	42.1	246	2 T24493	hypothetical prote
17	116	40.7	425	2 C89753	protein FilC7.3 fi
18	113	39.6	173	2 S47171	Gene PR-1 protein
19	112	39.3	299	2 S56031	pathogenesis-relat
20	111.5	39.1	167	2 S51679	pathogenesis-relat
21	111.5	39.1	245	2 S68691	neutrophil granule
22	109	38.2	243	2 B33329	cysteine-rich secr
23	108.5	38.1	212	2 T22437	hypothetical prote
24	107	37.5	161	2 E83534	PR-1-like protein
25	106.5	37.4	179	2 S23531	pathogenesis-relat
26	106.5	37.4	312	2 T16415	hypothetical prote
27	106	37.2	262	2 T24854	hypothetical prote
28	105.5	37.0	159	2 S26238	pathogenesis-relat
29	105	36.8	210	2 T04233	pathogenesis-relat

30	102.5	36.0	168	2 A24620	pathogenesis-relat
31	102.5	36.0	177	2 T08126	pathogenesis-relat
32	101.5	35.6	159	1 VCT014	pathogenesis-relat
33	101.5	35.6	207	2 T22438	hypothetical prote
34	101	35.4	208	2 T19852	hypothetical prote
35	100.5	35.3	184	2 S10205	pathogenesis-relat
36	99.5	34.9	177	2 S04728	pathogenesis-relat
37	99.5	34.9	190	2 T04232	pathogenesis-relat
38	99	34.7	208	2 T20661	hypothetical prote
39	99	34.7	329	2 S38082	pathogenesis-relat
40	98.5	34.6	163	2 T04989	pathogenesis-relat
41	98.5	34.6	219	2 JC4131	glioma pathogenesi
42	98.5	34.6	266	2 JC5308	testis-specific, v
43	98	34.4	205	2 T48294	pathogenesis relat
44	98	34.4	207	2 T22436	hypothetical prote
45	97	34.0	176	2 F94583	pathogenesis-relat

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A>Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol.
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 97.2%; Score 277; DB 2; Length 204;
Best Local Similarity 95.9%; Pred. No. 2.9e-27;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTQWVWANTKEVGGSGIKYIOEKWHKHYLVNCYGPGSNFKNEELYQTK 49
DB 156 HYTQWVWANTKEVGGSGIKFIQEKWHKHYLVNCYGPGSNFKNEELYQTK 204

RESULT 2

B37329
antigen 5 - eastern yellowjacket
C:Species: Vespula maculifrons (eastern yellowjacket)
C>Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B37329
R:Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
Submitted to the Protein Sequence Database, August 1992
A:Reference number: A37329
A:Accession: B37329
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <LUI>
A:Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 96.8%; Score 276; DB 2; Length 204;
Best Local Similarity 95.9%; Pred. No. 3.9e-27;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTQWVWANTKEVGGSGIKYIOEKWHKHYLVNCYGPGSNFKNEELYQTK 49
DB 156 HYTQWVWANTKEVGGSGIKYIOEKWHKHYLVNCYGPGSNFKNEELYQTK 204

RESULT 3

XX SQ Sequence 49 AA;
 Query Match 100.0%; Score 285; DB 5; Length 49;
 Best Local Similarity 100.0%; Pred. No. 5.3e-32;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
 Db 1 HYTMWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49

RESULT 2
 AAY45217
 ID AAY45217 standard; protein; 204 AA.
 XX AC AAY45217;
 XX DT 05-JAN-2000 (first entry)
 XX DE Wild type wasp Ves v 5 protein sequence.
 XX KW Bet v 1; Ves v 5; pollen allergen; Fagales; Oleales; Piniales; mutant;
 XX KW Hymenoptera; IGE; immunoglobulin E; vaccine; allergic reaction.
 XX OS Vespula lewisii.
 XX PN WO9947680-A1.
 XX PD 23-SEP-1999.
 XX PF 16-MAR-1999; 99WO-DK000136.
 XX PR 16-MAR-1998; 98DK-00000364.
 XX PA (ALKA-) ALK-ABELLO AS.
 XX PI Ipsen HH, Spangfort MD, Larsen JN;
 XX DR WPI; 1999-601103/51.
 XX DR N-PSDB; AAZ25685.
 XX PT New mutated allergen with lower specific affinity to IGE, useful for
 treatment of allergic reactions.
 XX PS Example 1; Fig 13; 77pp; English.
 XX CC The present invention describes a recombinant mutated allergen, with a
 surface exposed substituted amino acid on a B-cell epitope. The
 recombinant, non-natural, mutated allergen has at least one surface-
 exposed conserved amino acid of a B-cell epitope substituted by another
 amino acid, and essentially the same alpha-carbon backbone tertiary
 structure as the naturally occurring allergen. The substituted amino acid
 does not occur in the same position of any known homologous protein
 within the taxonomic order of the natural allergen. Specific IGE binding
 to the mutant is reduced compared to the naturally occurring allergen.
 The recombinant allergen is used as a vaccine to treat, prevent or
 alleviate allergic reactions. The present sequence represents the wild
 type Ves v 5, which can have the following mutations: Lys72Ala and
 Tyr96Ala
 XX SQ Sequence 204 AA;
 Query Match 100.0%; Score 285; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.9e-31;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
 Db 156 HYTMWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204

RESULT 3

ABG66977
 ID ABG66977 standard; protein; 204 AA.
 XX AC ABG66977;
 XX DT 24-SEP-2002 (first entry)
 XX DE Wasp venom antigen 5 mutant K29A.
 XX KW Immunoglobulin E; IGE; allergen; allergy; mite; hay fever;
 KW rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
 KW vaccine; antiallergic; B cell epitope.
 XX OS Vespula vulgaris.
 XX PN WO200240676-A2.
 XX PD 23-MAY-2002.
 XX PF 16-NOV-2001; 2001WO-DK000764.
 XX PR 16-NOV-2000; 2000DK-00001718.
 XX PR 16-NOV-2000; 2000US-024936P.
 XX PR 14-JUN-2001; 2001US-0298170P.
 XX PA (ALKA-) ALK-ABELLO AS.
 XX PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
 XX DR WPI; 2002-508328/54.
 XX PT New recombinant mutant allergen, useful for preventing and/or treating
 allergy, comprises multiple mutations and reduced immunoglobulin E
 binding affinity.
 XX PS Example 3; Page: 210pp; English.
 XX CC The invention relates to a recombinant allergen (I) which is a mutant of
 a naturally occurring allergen, where the mutant allergen has at least
 four primary mutations, which each reduce the specific immunoglobulin E
 (IGE) binding capability of the mutated allergen as compared to the IGE
 binding capability of the naturally occurring allergen, where each
 primary mutation is a substitution of one surface-exposed amino acid
 residue with another residue, which does not occur in the same position
 in the amino acid sequence of any known homologous protein within the
 taxonomic species from which the naturally occurring allergen originates,
 and each primary mutation is spaced from each other primary mutation by
 at least 15 Angstrom, and the primary mutations are placed in such a
 manner that at least one circular surface region with a area of 800
 Angstrom² comprises no mutation. Also included are a composition
 comprising two or more of the recombinant allergens, where the variant
 allergen is defined by having at least one primary mutation, which is
 absent in at least one of the other variants, and for each variant no
 secondary mutation is present within a radius of 15 Angstrom from each
 absent primary mutation; a DNA sequence encoding the recombinant allergen
 or its derivative, partial sequence or degenerated sequence, where the
 sequence which hybridises to it under stringent conditions, where the
 derivative, partial sequence, degenerated sequence or hybridising
 sequence encodes a peptide having at least one B cell epitope; an
 expression vector comprising the DNA and a host cell comprising the
 vector. The recombinant allergen is useful as a pharmaceutical, for
 preparing a pharmaceutical for preventing and/or treating allergy, or in
 a diagnostic assay for assessing relevance, safety or outcome of therapy
 of a subject, where an IGE containing sample of the subject is mixed with
 the recombinant allergen and assessed for the level of reactivity between
 the IGE in the sample and the recombinant allergen. The recombinant
 allergen or compositions are useful for generating an immune response in
 a subject, for vaccination or treatment of a subject or for the
 treatment, prevention or alleviation of allergic reactions in a subject
 e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
 anaphylaxis. The present sequence represents a recombinant allergen of
 the invention. Note: The present sequence was not shown in the

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 68.2634 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-8

Perfect score: 285

Sequence: 1 HYTQMVMANTKEVCGSIRY.....LVCNYGSPGNKBNELYQTK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	285	100.0	49	AAE28814	Aae28814 Vesputa v
2	285	100.0	204	AAV45217	Aay45217 Wild type
3	285	100.0	204	ABG66977	Abg66977 Wasp veno
4	285	100.0	204	ABG66983	Abg66983 Wasp veno
5	285	100.0	204	ABG67052	Abg67052 Wasp veno
6	285	100.0	204	ABG67104	Abg67104 Wasp veno
7	285	100.0	204	ABG67103	Abg67103 Wasp veno
8	285	100.0	204	AAE28820	Aae28820 Vesputa v
9	285	100.0	209	ABM00031	Abm00031 Allergen
10	279	97.9	204	AAW35688	Aaw35688 Vespid an
11	279	97.9	227	AAE25644	Aay25644 Vesputa v
12	279	97.9	227	AAE13071	Aae13071 Vesputa v
13	279	97.9	227	ADC34893	Adc34893 Wasp alle
14	276	96.8	204	AAW35687	Aaw35687 Vespid an
15	237	83.2	206	AAE25648	Aay25648 Vesputa s
16	237	83.2	206	ADC34897	Adc34897 Wasp alle
17	226	79.3	203	AAW35689	Aaw35689 Vespid an
18	217	76.1	205	AAW35690	Aaw35690 Vespid an
19	210	73.7	204	AAW35691	Aaw35691 Vespid an
20	203	71.2	125	AAV44015	Aay44015 White-fac
21	196	68.8	124	AAV44014	Aay44014 White-fac
22	189	66.3	205	AAW35693	Aaw35693 Vespid an
23	181	63.5	205	AAW35692	Aaw35692 Vespid an
24	181	63.5	205	AAE28821	Aae28821 Pollistes

25	158.5	55.6	162	5	AAE21099	Aae21099 Human spe
26	135	47.4	172	4	ABU53238	Abu53238 Human tes
27	133.5	46.8	202	9	ADY66414	Ady66414 S. mangon
28	123	43.2	20	2	AAW35678	Aaw35678 T. cell pe
29	123	43.2	225	8	ADP43676	Adp43676 Human PMM
30	123	43.2	266	4	AAW39716	Aaw39716 Human pol
31	123	43.2	270	2	AAW63115	Aaw63115 A human p
32	123	43.2	270	6	ABU92021	Abu92021 Human pro
33	123	43.2	270	8	ADP07714	Adp07714 Human sec
34	123	43.2	270	8	ADQ65201	Adq65201 Novel hum
35	123	43.2	347	4	AAW41502	Aaw41502 Human pol
36	123	43.2	347	7	ADAE08995	Ada08995 Novel pro
37	123	43.2	347	7	ADE10009	Ade10009 Novel pro
38	123	43.2	463	2	AAV13392	Aav13392 Amino aci
39	123	43.2	463	3	AAW01373	Aaw01373 Neuron-as
40	123	43.2	463	3	AAV95343	Aav95343 Human PRO
41	123	43.2	463	3	ADC78597	Adc78597 Human PRO
42	123	43.2	463	4	AAW80260	Aaw80260 Human PRO
43	123	43.2	463	4	AAU12351	Aau12351 Human ang
44	123	43.2	463	4	AAW53088	Aaw53088 Human ang
45	123	43.2	463	4	AAW88408	Aaw88408 Human mem

ALIGNMENTS

RESULT 1
AAE28814
ID AAE28814 standard; peptide; 49 AA.
XX
AC AAE28814;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #8.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
N-PSDB; RAD46232.
XX
New allergen hybrid protein having reduced allergenicity but retaining immunogenicity, useful for treating allergy or immune system related diseases.
XX
Claim 17; Page 151; 222pp; English.
XX
The present invention relates to recombinant allergen hybrid proteins having reduced allergenicity but retaining immunogenicity. The hybrid proteins comprise a peptide epitope sequence of an allergen protein and a scaffold protein that is structurally homologous to the allergen protein. Sequences of the invention comprise a native conformation and the peptide epitope sequence is present in a surface accessible region of the hybrid protein corresponding to its position in the allergen protein. The hybrid proteins are useful for treating allergy or immune system related diseases. They are also used as vaccines. The present sequence is Vesputa vulgaris antigen 5 (Ves V5) allergen peptide

Wed Apr 19 09:09:58 2006

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; ORGANISM: Homo sapiens
US-10-453-372-98

Query Match      24.5%; Score 62.5; DB 6; Length 475;
Best Local Similarity 43.8%; Pred. No. 2.6;
Matches 14; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 VQONVALTGSTAAYDDPVKLVKQWDEVDKY 48
Db 111 VQONIAKRSTTAALFDSFGKLVKQWENEVKDFNPNLEWSKNLKKTG 157

RESULT 3
US-11-090-439-38
; Sequence 38, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel P.
; APPLICANT: Weiner, Michael P.
; TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
; TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
; FILE REFERENCE: 24318-52
; CURRENT APPLICATION NUMBER: US/11/090,439
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/556,344
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-439-38

Query Match      27.3%; Score 69.5; DB 7; Length 258;
Best Local Similarity 40.9%; Pred. No. 0.16;
Matches 18; Conservative 8; Mismatches 5; Indels 13; Gaps 3;

QY 2 VQONVAL-TGSTAAYDDPVKLVKQWDEVDKY-----NPK 36
Db 121 LGQNLVSTG-----RYRSILQLVQWYDEVDKYAFPPQDCNFR 160

RESULT 4
US-10-453-372-98
; Sequence 98, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90

Query Match      24.5%; Score 62.5; DB 6; Length 477;
Best Local Similarity 43.8%; Pred. No. 2.7;
Matches 14; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 VQONVALTGSTAAYDDPVKLVKQWDEVDKY 33
Db 110 IGQNL---GAHWGRYRSPGFHVQSWYDEVDKY 138

RESULT 6
US-10-453-372-92
; Sequence 92, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90
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; ORGANISM: Homo sapiens
US-10-453-372-98

Query Match      24.5%; Score 62.5; DB 6; Length 475;
Best Local Similarity 43.8%; Pred. No. 2.6;
Matches 14; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 VQONVALTGSTAAYDDPVKLVKQWDEVDKY 33
Db 88 IGQNL---GAHWGRYRSPGFHVQSWYDEVDKY 116

RESULT 5
US-10-453-372-90
; Sequence 90, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 90
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90

Query Match      24.5%; Score 62.5; DB 6; Length 477;
Best Local Similarity 43.8%; Pred. No. 2.7;
Matches 14; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 VQONVALTGSTAAYDDPVKLVKQWDEVDKY 33
Db 110 IGQNL---GAHWGRYRSPGFHVQSWYDEVDKY 138

RESULT 6
US-10-453-372-92
; Sequence 92, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 92
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 11.9084 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKFSGNDFLKTG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
5: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES										
Result No.	Score	Query Match	Length	ID	Description					
1	255	100.0	227	6	US-10-498-026-76	Sequence 76, Appl				
2	148	58.0	206	6	US-10-498-026-80	Sequence 80, Appl				
3	69.5	27.3	258	7	US-11-090-439-38	Sequence 38, Appl				
4	62.5	24.5	475	6	US-10-453-372-98	Sequence 98, Appl				
5	62.5	24.5	477	6	US-10-453-372-90	Sequence 90, Appl				
6	62.5	24.5	497	6	US-10-453-372-92	Sequence 92, Appl				
7	62.5	24.5	497	6	US-10-453-372-100	Sequence 100, Appl				
8	62.5	24.5	497	6	US-10-453-372-102	Sequence 102, Appl				
9	62.5	24.5	497	6	US-10-218-784-56	Sequence 56, Appl				
10	62.5	24.5	497	6	US-10-219-061-56	Sequence 56, Appl				
11	62.5	24.5	497	6	US-10-219-062-56	Sequence 56, Appl				
12	62.5	24.5	497	6	US-10-219-064-56	Sequence 56, Appl				
13	62.5	24.5	497	6	US-10-233-134-56	Sequence 56, Appl				
14	62.5	24.5	501	6	US-10-453-372-96	Sequence 96, Appl				
15	61.5	24.1	500	6	US-10-194-487-70	Sequence 70, Appl				
16	61.5	24.1	500	6	US-10-195-883-70	Sequence 70, Appl				
17	61.5	24.1	500	6	US-10-195-888-70	Sequence 70, Appl				
18	61.5	24.1	500	6	US-10-195-889-70	Sequence 70, Appl				
19	61.5	24.1	500	7	US-11-067-573-2	Sequence 2, Appl				
20	58	22.7	76	7	US-11-078-463-8214	Sequence 8214, Ap				
21	58	22.7	379	7	US-11-096-568A-26485	Sequence 26485, A				
22	58	22.7	397	7	US-11-096-568A-26484	Sequence 26484, A				
23	58	22.7	413	7	US-11-096-568A-26483	Sequence 26483, A				
24	58	22.7	498	6	US-10-453-372-94	Sequence 94, Appl				
25	57.5	22.5	572	7	US-11-188-298-19935	Sequence 19935, A				

26	57	22.4	446	7	US-11-188-298-17336	Sequence 17336, A
27	55.5	21.8	572	7	US-11-188-298-7715	Sequence 7715, Ap
28	54.5	21.4	574	7	US-11-188-298-6884	Sequence 6884, Ap
29	54.5	21.4	574	7	US-11-188-298-18570	Sequence 18570, A
30	54.5	21.4	636	7	US-11-079-463-6686	Sequence 6686, Ap
31	54	21.2	476	7	US-11-096-568A-6988	Sequence 6988, Ap
32	54	21.2	486	7	US-11-096-568A-6987	Sequence 6987, Ap
33	54	21.2	566	7	US-11-096-568A-6986	Sequence 6986, Ap
34	54	21.2	678	7	US-11-188-298-11543	Sequence 11543, A
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36	53.5	21.0	373	7	US-11-096-568A-30166	Sequence 30166, A
37	53.5	21.0	422	7	US-11-096-568A-30165	Sequence 30165, A
38	53.5	21.0	574	7	US-11-024-959-300	Sequence 300, App
39	53	20.8	278	7	US-11-188-298-15868	Sequence 15868, A
40	52.5	20.6	210	7	US-11-096-568A-14899	Sequence 14899, A
41	52.5	20.6	264	7	US-11-096-568A-14898	Sequence 14898, A
42	52.5	20.6	423	6	US-10-506-454-247	Sequence 247, App
43	52.5	20.6	607	7	US-11-188-298-834	Sequence 834, App
44	52	20.4	120	7	US-11-152-846-7	Sequence 7, Appli
45	52	20.4	120	7	US-11-183-205-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76
Query Match 100.0%; Score 255; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVGQNVALTGSTAAKYDDPVKLVKRWWEDEVKDYNPKKKFSGNDFLKTG 48
Db 131 QVGQNVALTGSTAAKYDDPVKLVKRWWEDEVKDYNPKKKFSGNDFLKTG 178
RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80
Query Match 58.0%; Score 148; DB 6; Length 206;
Best Local Similarity 59.6%; Pred. No. 7.6e-12;
Matches 28; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

ORGANISM: Vesputa vulgaris
US-10-091-135-16
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 155
RESULT 3
US-10-091-135-64
Sequence 64, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 204
TYPE: PRT
ORGANISM: Vesputa vulgaris
US-10-091-135-64
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 155
RESULT 4
US-10-091-135-81
Sequence 81, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 204
TYPE: PRT
ORGANISM: Vesputa vulgaris
US-10-091-135-81
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 155

RESULT 5
US-10-719-553-39
Sequence 39, Application US/10719553
Publication No. US20040091500A1
GENERAL INFORMATION:
APPLICANT: Ipsen, Hans Henrik
APPLICANT: Spangfort, Michael Dho
APPLICANT: Larsen Jorgen Nedergaard
TITLE OF INVENTION: NOVEL RECOMBINANT ALLERGENS
FILE REFERENCE: 04305/100E144-US2
CURRENT APPLICATION NUMBER: US/10/719,553
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 09/270,910
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/078,371
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 204
TYPE: PRT
ORGANISM: vesputa vulgaris
US-10-719-553-39
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 155
RESULT 6
US-09-957-806A-22
Sequence 22, Application US/09957806A
Publication No. US20050181446A1
GENERAL INFORMATION:
APPLICANT: Roggen, Erwin
APPLICANT: Ernst, Steffen
APPLICANT: Svendsen, Allan
APPLICANT: Friis, Esben
APPLICANT: Oeten, Claus
TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
FILE REFERENCE: 10021.204-US
CURRENT APPLICATION NUMBER: US/09/957,806A
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 209
TYPE: PRT
ORGANISM: Vesputa vulgaris
US-09-957-806A-22
Query Match 100.0%; Score 255; DB 3; Length 209;
Best Local Similarity 100.0%; Pred. No. 9.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 48
DB 113 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFSGNDPLKGTG 160
RESULT 7
US-10-001-245-214
Sequence 214, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 73.4657 Seconds
(without alignments)
272.996 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKKFSGNDFLKTG 48

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	255	100.0	204	4	US-10-091-135-64
4	255	100.0	204	4	US-10-091-135-81
5	255	100.0	204	4	US-10-719-533-39
6	255	100.0	209	3	US-09-957-806A-22
7	255	100.0	210	4	US-10-001-245-214
8	255	100.0	227	3	US-09-847-208-170
9	255	100.0	227	5	US-10-809-689-82
10	250	98.0	204	3	US-09-847-208-162
11	250	98.0	204	4	US-10-091-135-65
12	244	95.7	202	4	US-10-001-245-117
13	244	95.7	203	4	US-10-001-245-118
14	227.5	89.2	201	4	US-10-001-245-119
15	226	88.6	204	3	US-09-847-208-163
16	226	88.6	204	4	US-10-091-135-67
17	224	87.8	204	3	US-09-847-208-165
18	224	87.8	204	4	US-10-091-135-63
19	213	83.5	204	3	US-09-847-208-166
20	213	83.5	204	4	US-10-091-135-66
21	208	81.6	198	4	US-10-001-245-121
22	193.5	72.0	192	4	US-10-001-245-122
23	174	68.2	194	4	US-10-001-245-120
24	148	58.0	206	3	US-09-847-208-171
25	148	58.0	206	4	US-10-091-135-68
26	148	58.0	206	5	US-10-809-689-86
27	136	53.3	203	3	US-09-847-208-86

28	136	53.3	203	4	US-10-091-135-71	Sequence 71, Appl
29	133.5	52.4	205	4	US-10-091-135-72	Sequence 72, Appl
30	133.5	52.4	215	3	US-09-847-208-91	Sequence 91, Appl
31	132	51.8	204	4	US-10-091-135-70	Sequence 70, Appl
32	132	51.8	205	3	US-09-847-208-167	Sequence 167, App
33	132	51.8	205	4	US-10-091-135-69	Sequence 69, Appl
34	132	51.8	227	3	US-09-847-208-90	Sequence 90, Appl
35	112	43.9	205	3	US-09-847-208-152	Sequence 152, App
36	112	43.9	205	4	US-10-091-135-76	Sequence 76, Appl
37	103	40.4	205	3	US-09-847-208-151	Sequence 151, App
38	103	40.4	205	4	US-10-091-135-77	Sequence 77, Appl
39	101.5	39.8	202	3	US-09-847-208-160	Sequence 160, App
40	101.5	39.8	202	4	US-10-091-135-74	Sequence 74, Appl
41	99.5	39.0	206	3	US-09-847-208-150	Sequence 150, App
42	98	38.4	205	4	US-10-091-135-17	Sequence 17, Appl
43	98	38.4	205	3	US-10-091-135-78	Sequence 78, Appl
44	98	38.4	209	3	US-09-847-208-149	Sequence 149, App
45	96.5	37.8	202	3	US-09-847-208-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-10-091-135-7
; Sequence 7, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGI
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-091-135-7

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Best Local Similarity	100.0%	Pred. No. 1.7e-26;		
Matches	48;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-091-135-16
; Sequence 16, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGI
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 204
; TYPE: PRT

Qy 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155

RESULT 2
US-08-614-935-2
; Sequence 2, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,287
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
; US-09-130-287-2

Query Match 100.0%; Score 255; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155

RESULT 4
US-09-541-759-6
; Sequence 6, Application US/09541759
; Patent No. 6723322
; GENERAL INFORMATION:
; APPLICANT: Lustigman, Sara
; APPLICANT: Pearlman, Eric
; APPLICANT: Unnasch, Thomas
; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
; FILE REFERENCE: 63475/252
; CURRENT APPLICATION NUMBER: US/09/541,759
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vesputula vulgaris
; US-09-541-759-6

Query Match 100.0%; Score 255; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155

RESULT 2
US-08-614-935-2
; Sequence 2, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
; US-08-614-935-2

Query Match 100.0%; Score 255; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGSTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155

RESULT 3
US-09-130-287-2
; Sequence 2, Application US/09130287
; Patent No. 6106844
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKKFSGNDFLKTG 48

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4: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255	100.0	204	1	US-08-419-414-9 Sequence 9, Appli
2	255	100.0	204	1	US-08-614-935-2 Sequence 2, Appli
3	255	100.0	204	2	US-09-130-287-2 Sequence 2, Appli
4	255	100.0	227	2	US-09-541-759-6 Sequence 6, Appli
5	224	87.8	204	1	US-08-614-935-1 Sequence 1, Appli
6	224	87.8	204	2	US-09-130-287-1 Sequence 1, Appli
7	136	53.3	203	1	US-08-419-414-8 Sequence 8, Appli
8	136	53.3	203	1	US-08-614-935-3 Sequence 3, Appli
9	136	53.3	203	2	US-09-130-287-3 Sequence 3, Appli
10	133.5	52.4	125	1	US-07-857-2248-114 Sequence 114, App
11	132.5	52.0	205	1	US-08-614-935-4 Sequence 4, Appli
12	132.5	52.0	205	2	US-09-130-287-4 Sequence 4, Appli
13	132	51.8	124	1	US-07-857-2248-113 Sequence 113, App
14	132	51.8	166	2	US-08-614-935-30 Sequence 30, Appl
15	132	51.8	166	2	US-09-130-287-30 Sequence 30, Appl
16	132	51.8	204	1	US-08-614-935-5 Sequence 5, Appli
17	132	51.8	204	2	US-09-130-287-5 Sequence 5, Appli
18	103	40.4	205	1	US-08-614-935-7 Sequence 7, Appli
19	98	38.4	205	2	US-08-419-414-10 Sequence 10, Appli
20	98	38.4	205	1	US-08-614-935-6 Sequence 6, Appli
21	98	38.4	205	2	US-09-130-287-6 Sequence 6, Appli
22	98	38.2	25	1	US-08-614-935-69 Sequence 69, Appl
23	82	32.2	25	1	US-08-614-935-69 Sequence 69, Appl
24	82	32.2	25	2	US-09-130-287-69 Sequence 20, Appl
25	65	25.5	20	1	US-08-614-935-20 Sequence 20, Appl
26	65	25.5	20	2	US-09-130-287-20 Sequence 20, Appl
27	63	24.7	25	1	US-08-614-935-68 Sequence 68, Appl

Sequence 68, Appli
Sequence 363, App
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Sequence 4, Appli
Sequence 4, Appli
Sequence 5968, Ap
Sequence 5967, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 8086, Ap
Sequence 11049, A
Sequence 19, Appl
Sequence 19, Appl
Sequence 30, Appl
Sequence 19047, A
Sequence 4966, Ap
Sequence 789, App
Sequence 789, App

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63 61.5 61.5 59 59 57 57 57 57 57 56 56 56 56 56 55.5 55.5 55.5

24.7 24.1 24.1 23.1 23.1 22.4 22.4 22.4 22.4 22.4 22.0 22.0 22.0 22.0 21.8 21.8 21.8

25 2 2 500 500 108 108 69 106 108 108 20 20 369 394 122 200 200

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US-10-020-445A-363
US-08-828-239-4
US-09-205-679-4
US-09-513-999C-5968
US-09-513-999C-5967
US-08-828-239-3
US-09-205-679-3
US-09-513-999C-8086
US-09-949-016-11049
US-08-614-935-19
US-09-130-287-19
US-03-668-097A-30
US-09-248-796A-19047
US-09-513-999C-4966
US-09-702-705-789
US-09-736-457-789

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Babst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/419,414
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Babst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
US-08-419-414-9

Query Match 100.0%; Score 255; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FT DISULFID 31 124 By similarity.
FT FT DISULFID 49 117 By similarity.
FT FT DISULFID 193 210 By similarity.
FT CONFLICT 109 109 V -> I (in Ref. 2).
FT CONFLICT 118 118 Q -> E (in Ref. 2).
FT CONFLICT 173 173 D -> N (in Ref. 2).
FT CONFLICT 219 219 M -> K (in Ref. 2).
FT HELIX 26 28
FT TURN 32 33
FT TURN 38 41
FT HELIX 38 41
FT STRAND 53 57
FT HELIX 61 79
FT TURN 80 81
FT TURN 87 88
FT STRAND 94 94
FT STRAND 101 102
FT STRAND 104 114
FT TURN 115 116
FT STRAND 133 141
FT HELIX 149 157
FT HELIX 158 162
FT TURN 165 166
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FT STRAND 226 227
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Query Match 100.0%; Score 255; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVGQNVALTGSTAAKYDDPVKLVKQWEDEVKYNPKKFSGNDPLKGTG 48
DB 131 QVGQNVALTGSTAAKYDDPVKLVKQWEDEVKYNPKKFSGNDPLKGTG 178

RESULT 2
VA5 VESFL STANDARD; PRT; 204 AA.
AC P35783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves f 5) (Ves f V).
OS Vespula flavopilosa (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30211;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; B44583; B44583.
CC HSP; Q05110; IQNX.
CC SMR; P35784; 1-204.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PR00837; V5TPXLKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A44583; A44583.
CC HSP; Q05110; IQNX.
CC SMR; P35783; 1-204.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PR00837; V5TPXLKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; CRISP_1; 1.
CC PROSITE; PS01010; CRISP_2; 1.
CC Allergen; Direct protein sequencing.
KW Allergen; By similarity.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 101 By similarity.
FT DISULFID 26 94 By similarity.
FT DISULFID 170 187 By similarity.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;

Query Match 98.0%; Score 250; DB 1; Length 204;
Best Local Similarity 97.9%; Pred. NO. 1.2e-22;
Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVGQNVALTGSTAAKYDDPVKLVKQWEDEVKYNPKKFSGNDPLKGTG 48
DB 108 QVGQNVALTGSTAAKYDDPVKLVKQWEDEVKYNPKKFSGNDPLKGTG 155

RESULT 3
VA5 VESGE STANDARD; PRT; 204 AA.
AC P35784;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves g 5) (Ves g V).
OS Vespula germanica (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30212;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; B44583; B44583.
CC HSP; Q05110; IQNX.
CC SMR; P35784; 1-204.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PR00837; V5TPXLKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 70.9008 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
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Scoring table: BLOSUM62
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Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255	100.0	227	1 VA5_VESVU	Q05110 vespula vul
2	250	98.0	204	1 VA5_VESFL	P35783 vespula fla
3	226	88.6	204	1 VA5_VESGE	P35784 vespula ger
4	224	87.8	204	1 VA5_VESMC	P35760 vespula mac
5	213	83.5	204	1 VA5_VESPE	P35785 vespula pen
6	148	58.0	206	1 VA5_VESVI	P35787 vespula vid
7	136	53.3	203	1 VA5_DOLAR	Q05108 dolichovesp
8	133.5	52.4	215	1 VA53_DOLMA	P10737 dolichovesp
9	132	51.8	205	1 VA5_VESQ	P35786 vespula equ
10	132	51.8	227	1 VA52_DOLMA	P10736 dolichovesp
11	112	43.9	205	1 VA5_POLFU	P35780 polistes fu
12	110.5	43.3	207	1 VA5_POLSR	Q72156 polybia scu
13	103	40.4	205	1 VA5_POLEX	P35759 polistes ex
14	103	40.4	226	2 Q68KJ9_POLEX	Q68KJ9 polistes ex
15	101.5	39.8	202	1 VA51_VESCR	P35781 vespa crabr
16	99.5	39.0	206	1 VA5_POLDO	P81656 polistes do
17	99.5	39.0	206	1 VA5_POLGA	P83377 polistes ga
18	99.5	39.0	227	2 Q68KJ8_POLDO	Q68KJ8 polistes do
19	98	38.4	209	1 VA5_POLAN	Q05109 polistes an
20	96.5	37.8	202	1 VA52_VESCR	P35782 vespa crabr
21	95	37.3	202	1 VA5_VESMA	P81657 vespa manda
22	80	31.4	234	1 VA3_SOLIN	P35778 solenopsis
23	71.5	28.0	280	2 Q7T141_BRARE	Q7T141 brachydanio
24	71.5	28.0	896	2 Q9FJ23_ARATH	Q9FJ23 arabidopsis
25	70.5	27.6	205	2 Q4S1C8_TETNG	Q4S1C8 tetraodon n
26	69.5	27.3	258	2 Q43692_HUMAN	Q43692 homo sapien
27	69.5	27.3	258	2 Q99MM7_MOUSE	Q99MM7 mus musculu
28	69.5	27.3	258	2 Q98ST6_CHICK	Q98ST6 gallus gall
29	69.5	27.3	269	2 Q8BS03_MOUSE	Q8BS03 mus musculu
30	69.5	27.3	295	2 Q4SMW6_TETNG	Q4SMW6 tetraodon n
31	69.5	27.3	360	2 Q75FB0_ASHGO	Q75FB0 ashbya goss

32	66.5	26.1	473	2	Q4SMW7_TETNG	Q4SMW7 tetraodon n
33	66	25.9	211	1	VA3_SOLRI	P35779 solenopsis
34	65.5	25.7	500	2	Q4V9Y5_XENTR	Q4V9Y5 xenopus tro
35	64	25.1	1005	2	Q6N602_RHOPA	Q6N602 rhodopseudo
36	63.5	24.9	619	2	Q8UE28_AGRTS	Q8UE28 agrobacteri
37	63.5	24.9	637	2	Q7CYW3_AGRTS	Q7CYW3 agrobacteri
38	63	24.7	107	2	Q4RY34_TETNG	Q4RY34 tetraodon n
39	63	24.7	112	2	Q6NYF7_BRARE	Q6NYF7 brachydanio
40	63	24.7	260	2	Q7Z0B5_STOCA	Q7Z0B5 stomoxys ca
41	63	24.7	846	2	Q5Y818_9BACT	Q5Y818 chrysogene
42	63	24.7	938	2	Q600F3_MYCHY	Q600F3 mycoplasma
43	62.5	24.5	258	2	Q6FSU9_CANGA	Q6FSU9 candida gla
44	62.5	24.5	316	2	Q6C9V2_YARLI	Q6C9V2 yarrowia li
45	62.5	24.5	371	2	Q96K61_HUMAN	Q96K61 homo sapien

ALIGNMENTS

RESULT 1
VA5_VESVU
ID - VA5_VESVU STANDARD; PRT; 227 AA.
AC Q05110; OSUB91;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (Ags) (Allergen Ves v 5) (Ves v V)
OS Vespula vulgaris (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7454;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93203603; PubMed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets.";
RL J. Immunol. 150:2823-2830(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 24-227.
RA Suck R., Hagen S., Fiebig H.;
RT "Molecular cloning of a genomic sequence from the venom allergen antigen 5 from Vespula vulgaris.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DR EMBL; M98858; AAA30333.1; -; mRNA.
DR EMBL; AJ238849; CAB42887.1; -; Genomic_DNA.
DR PDB; IQNX; X-ray; A=24-227.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00838; V5ALLERGEN.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; P000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; CRISP 1; 1.
DR PROSITE; PS01010; CRISP 2; 1.
KW 3D-structure; Allergen; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 227 Venom allergen 5.
FT DISULFID 27 40 By similarity.

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RESULT 3
B37329
antigen 5 - eastern yellowjacket
C/Species: Vespula maculifrons (eastern yellowjacket)
C/Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C/Accession: B37329
R;Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A/Reference number: A37329
A/Accession: B37329
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-204 <LUI>
A/Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C/Superfamily: yellowjacket venom allergen antigen 5

Query Match      87.8%; Score 224; DB 2; Length 204;
Best Local Similarity 89.6%; Pred. No. 3.9e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QVGNVALTGSTAAKYDDPVKLVKQWEDEVKDYNNPKKFKSGNDFLKTG 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 108 QVGNVALTGSTAAAYNDPVKLVKQWEDEVKDYNNPKKFKSENFLKIG 155

RESULT 4
C44583
venom allergen antigen Ves p 5 - western yellowjacket
C/Species: Vespula pensylvanica (western yellowjacket)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: C44583; C44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A/Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molec
A/Reference number: A44583; MUID:94044316; PMID:8227862
A/Accession: C44583
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-204 <HOF>
A/Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C/Superfamily: yellowjacket venom allergen antigen 5

Query Match      83.5%; Score 213; DB 2; Length 204;
Best Local Similarity 87.2%; Pred. No. 8.8e-19;
Matches 41; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QVGNVALTGSTAAKYDDPVKLVKQWEDEVKDYNNPKKFKSGNDFLKTG 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 109 QVGNVALTGSTADKYNDPVKLVKQWEDEVKDYNNPKKFKSENFNKIG 155

RESULT 5
E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C/Species: Vespula vidua
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: E44583; E44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A/Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molec
A/Reference number: A44583; MUID:94044316; PMID:8227862
A/Accession: E44583
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-206 <HOF>
A/Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C/Superfamily: yellowjacket venom allergen antigen 5

Query Match      58.0%; Score 148; DB 2; Length 206;
Best Local Similarity 59.6%; Pred. No. 9.2e-11;
Matches 28; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 2 QVGNVALTGSTAAKYDDPVKLVKQWEDEVKDYNNPKKFKSGNDFLKTG 48
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Db 111 VGNIAKRSTTAALFSDPSGKLVKQWENEVDKDFNPNIEWSQNLKKTG 157

RESULT 6
B31085
antigen 5-3 precursor - bald-faced hornet (fragment)
C/Species: Vespula maculata (bald-faced hornet)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: B31085
R;Fang, K.S.Y.; Vitale, M.; Fehlner, P.; King, T.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988
A/Title: cDNA cloning and primary structure of a white-face hornet venom allergen, ant
A/Reference number: A94213; MUID:88124947; PMID:3422469
A/Accession: B31085
A/Molecule type: mRNA
A/Residues: 1-213 <FAN>
A/Cross-references: UNIPROT:P10737; UNIPARC:UPI000017922B
C/Superfamily: yellowjacket venom allergen antigen 5
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-213/Product: antigen 5-3 #status predicted <NAT>

Query Match      52.0%; Score 132.5; DB 2; Length 213;
Best Local Similarity 55.1%; Pred. No. 7.7e-09;
Matches 27; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

Qy 1 QVGNVALTGSTAAKYDDPVKLVKQWEDEVKDYNNPKKFKSGNDFLKTG 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 118 QVGNVALIASTGNSVATWSKLIEMWENEVDKDFNPNIEWSQNLKKTG 166

RESULT 7
D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C/Species: Vespula squamosa (southern yellowjacket)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: D44583; D44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A/Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A/Reference number: A44583; MUID:94044316; PMID:8227862
A/Accession: D44583
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-205 <HOF>
A/Cross-references: UNIPROT:P35786; UNIPARC:UPI0000138094
C/Superfamily: yellowjacket venom allergen antigen 5

Query Match      51.8%; Score 132; DB 2; Length 205;
Best Local Similarity 53.2%; Pred. No. 8.6e-09;
Matches 25; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 2 VGNVALTGSTAAKYDDPVKLVKQWEDEVKDYNNPKKFKSGNDFLKTG 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 110 VGNIAVSSSTAAYENVGNLVKQWENEVDKDFNPNIEWSQNEFKKIG 156

RESULT 8
A31085
antigen 5-2 precursor - bald-faced hornet
C/Species: Vespula maculata (bald-faced hornet)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: A31085
R;Fang, K.S.Y.; Vitale, M.; Fehlner, P.; King, T.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988
A/Title: cDNA cloning and primary structure of a white-face hornet venom allergen, ant
A/Reference number: A94213; MUID:88124947; PMID:3422469
A/Accession: A31085
A/Molecule type: mRNA
A/Residues: 1-227 <FAN>
A/Cross-references: UNIPROT:P10736; UNIPARC:UPI000013807D; GB:J03601; NID:g156714; PID
C/Superfamily: yellowjacket venom allergen antigen 5
F;1-23/Domain: signal sequence #status predicted <SIG>
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 10.0763 Seconds
(without alignments)
459.342 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKFSGNDFLKTG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	98.0	204	2 A44583	venom allergen ant
2	226	88.6	204	2 B44583	venom allergen ant
3	224	87.8	204	2 B37329	antigen 5 - easter
4	213	83.5	204	2 C44583	venom allergen ant
5	148	58.0	206	2 E44583	venom allergen ant
6	132.5	52.0	213	2 B31085	antigen 5-3 precu
7	132	51.8	205	2 D44583	venom allergen ant
8	132	51.8	227	2 A31085	antigen 5-2 precu
9	112	43.9	205	2 F44583	venom allergen ant
10	103	40.4	205	2 A37329	antigen 5 - paper
11	101.5	39.8	202	2 H44583	venom allergen ant
12	96.5	37.8	202	2 H44583	venom allergen III
13	78	20.6	212	2 B37320	venom allergen Sol
14	66	25.9	211	2 B58853	poly-beta-hydroxyb
15	63.5	24.9	619	2 AH2773	hypothetical prote
16	63.5	24.9	637	2 F97553	hypothetical prote
17	62	24.3	273	2 AC1435	hypothetical prote
18	62	24.3	273	2 AD1077	hypothetical prote
19	61	23.9	761	2 S60992	cap-binding protei
20	60.5	23.7	206	2 JC5331	probable ubiquitin
21	60	23.5	1053	2 T06483	superfamily I DNA
22	60	23.5	1351	2 E97273	coupling factor 6
23	59	23.1	108	1 JLBO6	hypothetical prote
24	59	23.1	518	2 T24783	protein-tyrosine-p
25	58	22.7	1494	2 T14355	calcium binding pr
26	57.5	22.5	168	2 S62881	coupling factor 6
27	57	22.4	108	2 JT0563	hypothetical prote
28	57	22.4	184	2 E90335	site-specific DNA-
29	57	22.4	336	2 S04739	

30	57	22.4	411	2	T13315	hypothetical prote
31	57	22.4	457	2	T29116	hypothetical prote
32	57	22.4	1091	2	S33850	fibronectin-binding
33	56.5	22.2	925	2	G88175	protein T24H7.2 [i
34	56.5	22.2	1260	2	A87046	hypothetical prote
35	56	22.0	182	2	JQ1753	hypothetical prote
36	56	22.0	385	2	T27079	hypothetical prote
37	55.5	21.8	155	2	C86637	hypothetical prote
38	55.5	21.8	318	2	D72283	galactose-1-phosph
39	55.5	21.8	352	2	C92302	iron(III) ABC tran
40	55.5	21.8	531	1	PIWLHS	major capsid prote
41	55	21.6	436	2	A38145	invariant surface
42	55	21.6	484	2	S00757	deoxyribodipyrimid
43	55	21.6	506	2	F69867	two-component sens
44	55	21.6	639	2	T16648	hypothetical prote
45	54.5	21.4	216	2	T01687	translation initia

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
J. Hoffman, D.R.
R. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 98.0%; Score 250; DB 2; Length 204;
Best Local Similarity 97.9%; Pred. No. 2.4e-23;
Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPVKLVKQWEDEVKDYNPKKKFSGNDFLKTG 48
Db 108 QVGQNVALTGSTAAKYDDPVKLVKQWEDEVKDYNPKKKFSGNDFLKTG 155

RESULT 2

B44583
venom allergen antigen Ves g 5 - German yellowjacket
C:Species: Vespula germanica (German yellowjacket)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; A44522
J. Hoffman, D.R.
R. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 88.6%; Score 226; DB 2; Length 204;
Best Local Similarity 91.5%; Pred. No. 2.2e-20;
Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VGQNVALTGSTAAKYDDPVKLVKQWEDEVKDYNPKKKFSGNDFLKTG 48
Db 109 VGQNVALTGSTAAKYDDPVKLVKQWEDEVKDYNPKKKFSGNDFLKTG 155

```

XX SQ      Sequence 48 AA;
Query Match      100.0%; Score 255; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPDKLVKQWDEVDKYNPKKFSGNDPLKGTG 48
Db 1 QVGQNVALTGSTAAKYDDPDKLVKQWDEVDKYNPKKFSGNDPLKGTG 48

RESULT 2
AAW35688
ID AAW35688 standard; peptide; 204 AA.
XX
AC AAW35688;
XX
DT 13-MAY-1998 (first entry)
XX
DE Vespid antigen 5s from Vesputia vulgaris (yellowjacket).
XX
KW Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW vespid venom; white face hornet wasp; immunodominant peptide; T cell.
XX
OS Vesputia vulgaris.
XX
PN W09733910-A1.
XX
PD 18-SEP-1997.
XX
PF 11-MAR-1997; 97WO-US003753.
XX
PR 11-MAR-1996; 96US-00614935.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI King TP;
XX
DR WPI; 1997-470817/43.
XX
PT Vespid venom antigen 5 peptide fragments - useful to treat or diagnose
PT vespid venom sensitivity.
XX
PS Example 1; Fig 1; 73pp; English.
XX
CC This sequence represents vespid antigen 5s from yellowjacket. The
CC invention relates to peptides derived from vespid venom antigen 5 (VVS)
CC that are antigenic for T cell proliferation in mice immunised with VVS.
CC The peptides can be used to treat or diagnose vespid venom sensitivity
CC e.g. to Dolichovesputia maculata (white face hornet), Vesputia vulgaris
CC (yellowjacket), V. maculifrons (yellowjacket), D. arenaria (yellow
CC hornet), Polistes annularis (wasp), P. exclamans (wasp), V. crabro
CC (European hornet), V. flavopilosa (yellowjacket), V. germanica
CC (yellowjacket), V. pennsylvanica (yellowjacket), V. squamosa
CC (yellowjacket), V. vidua (yellowjacket) and P. fuscatus (paperwasp)
XX
SQ      Sequence 204 AA;
Query Match      100.0%; Score 255; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPDKLVKQWDEVDKYNPKKFSGNDPLKGTG 48
Db 108 QVGQNVALTGSTAAKYDDPDKLVKQWDEVDKYNPKKFSGNDPLKGTG 155

RESULT 3
AAW45217
ID AAW45217 standard; protein; 204 AA.
XX
AC AAW45217;

```

```

XX DT      05-JAN-2000 (first entry)
XX
DE Wild type wasp Ves v 5 protein sequence.
XX
KW Bet v 1; Ves v 5; pollen allergen; Fagales; Oleales; Pinales; mutant;
KW Hymenoptera; IgE; immunoglobulin E; vaccine; allergic reaction.
XX
OS Vesputia lewisii.
XX
PN W09947680-A1.
XX
PD 23-SEP-1999.
XX
PF 16-MAR-1999; 99WO-DK000136.
XX
PR 16-MAR-1998; 98DK-00000364.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Ipsen HH, Spangfort MD, Larsen JN;
XX
DR WPI; 1999-601103/51.
DR N-PSDB; AA225685.
XX
PT New mutated allergen with lower specific affinity to IgE, useful for
PT treatment of allergic reactions.
XX
PS Example 1; Fig 13; 77pp; English.
XX
CC The present invention describes a recombinant mutated allergen, with a
CC surface exposed substituted amino acid on a B-cell epitope. The
CC recombinant, non-natural, mutated allergen has at least one surface-
CC exposed conserved amino acid of a B-cell epitope substituted by another
CC amino acid, and essentially the same alpha-carbon backbone tertiary
CC structure as the naturally occurring allergen. The substituted amino acid
CC does not occur in the same position of any known homologous protein
CC within the taxonomic order of the natural allergen. Specific IgE binding
CC to the mutant is reduced compared to the naturally occurring allergen.
CC The recombinant allergen is used as a vaccine to treat, prevent or
CC alleviate allergic reactions. The present sequence represents the wild
CC type Ves v 5, which can have the following mutations: Lys72Ala and
CC Tyr96Ala
XX
SQ      Sequence 204 AA;
Query Match      100.0%; Score 255; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPDKLVKQWDEVDKYNPKKFSGNDPLKGTG 48
Db 108 QVGQNVALTGSTAAKYDDPDKLVKQWDEVDKYNPKKFSGNDPLKGTG 155

RESULT 4
ABG66977
ID ABG66977 standard; protein; 204 AA.
XX
AC ABG66977;
XX
DT 24-SEP-2002 (first entry)
XX
DE Wasp venom antigen 5 mutant K29A.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mite; hay fever;
KW rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Vesputia vulgaris.
XX
PS Synthetic.
XX
PN W0200240676-A2.

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 66.8702 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVCQNVALTGSTAAKYDDPV.....EVKDYNPKKKFSGNDFLKTG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255	100.0	48	AAE28813	Aae28813 Vesputa v
2	255	100.0	204	AAW35688	Aaw35688 Vespid an
3	255	100.0	204	AAy45217	Aay45217 Wild type
4	255	100.0	204	ABg66977	Abg66977 Wasp veno
5	255	100.0	204	ABg67052	Abg67052 Wasp veno
6	255	100.0	204	ABg67104	Abg67104 Wasp veno
7	255	100.0	204	ABg67103	Abg67103 Wasp veno
8	255	100.0	204	AAE28820	Aae28820 Vesputa v
9	255	100.0	209	ABM00031	Abm00031 Allergen
10	255	100.0	227	AAy25644	Aay25644 Vesputa s
11	255	100.0	227	AAE13071	Aae13071 Vesputa v
12	255	100.0	227	ADC34893	Adc34893 Wasp alle
13	249	97.6	204	ABg66983	Abg66983 Wasp veno
14	224	87.8	204	AAW35687	Aaw35687 Vespid an
15	148	58.0	206	AAy25648	Aay25648 Vesputa s
16	148	58.0	206	ADC34897	Adc34897 Wasp alle
17	136	53.3	203	AAW35689	Aaw35689 Vespid an
18	133.5	52.4	125	AAy44015	Aay44015 White-fac
19	132.5	52.0	205	AAW35690	Aaw35690 Vespid an
20	132	51.8	124	AAy44014	Aay44014 White-fac
21	132	51.8	204	AAW35691	Aaw35691 Vespid an
22	103	40.4	205	AAW35693	Aaw35693 Vespid an
23	98	38.4	205	AAW35692	Aaw35692 Vespid an
24	98	38.4	205	AAE28821	Aae28821 Polistes

25	92	36.1	162	5	AAE21099	Aae21099 Human epe
26	82	32.2	25	2	AAW35671	Aaw35671 T cell pe
27	78	30.6	172	4	ABU53238	Abu53238 Human tes
28	69.5	27.3	188	2	AAW79915	Aaw79915 Human try
29	69.5	27.3	198	2	AAW79914	Aaw79914 Trypsin i
30	69.5	27.3	258	3	AAW79301	Aaw79301 Protein e
31	69.5	27.3	258	5	ABG61801	Abg61801 Prostate
32	69.5	27.3	258	5	ABG61802	Abg61802 Prostate
33	69.5	27.3	258	5	ABJ05597	Abj05597 Breast ca
34	69.5	27.3	258	8	ADr14401	Adr14401 Human NF-
35	65.5	25.7	482	4	ABB62392	Abb62392 Drosophil
36	65.5	25.7	482	9	ADY79831	Ady79831 Amino aci
37	65	25.5	20	2	AAW35627	Aaw35627 Immunomod
38	64.5	25.3	205	8	ADx72834	Adx72834 Plant ful
39	63.5	24.9	96	8	ADN99462	Adn99462 Novel hum
40	63.5	24.9	142	4	AAU19527	Aau19527 Human dia
41	63	24.7	25	2	AAW35670	Aaw35670 T cell pe
42	62.5	24.5	241	4	AAW24028	Aaw24028 Rat EST e
43	62.5	24.5	252	5	ABB80591	Abb80591 Human ebg
44	62.5	24.5	371	4	AAW93979	Aaw93979 Human pro
45	62.5	24.5	438	5	ABB80593	Abb80593 Human ebg

ALIGNMENTS

RESULT 1
AAE28813
ID AAE28813 standard; peptide; 48 AA.
XX
AC AAE28813;
XX
DT 27-DEC-2002 (first entry)
XX
DE vesputa vulgaris antigen 5 (Ves V5) allergen peptide #7.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
FN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
FA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
N-PSDB; AAD46231.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 151; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide

Publication No. US20060024692A1
GENERAL INFORMATION:
APPLICANT: Nakamura, Yusuke
APPLICANT: Daigo, Yataro
APPLICANT: Nakatsuru, Shuichi
TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS
FILE REFERENCE: 082368-003500US
CURRENT APPLICATION NUMBER: US/11/090,617
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: PCT/JP04/04075
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: PCT/JP03/12072
PRIOR FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US 60/555,757
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: US 60/466,100
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/451,374
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/414,673
PRIOR FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 706
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 706
LENGTH: 2911
TYPE: PRT
ORGANISM: Homo sapiens
US-11-090-617-706

Query Match 26.4%; Score 58; DB 7; Length 2911;
Best Local Similarity 32.3%; Pred. No. 20;
Matches 10; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

QY 4 CKIKCKLGGV-----HTACKYGSCLKPNCNKV 30
DB 149 CSVRCHNGGTCAADHCCQCKGYIGTYCGQPV 179

RESULT 6
US-11-108-528-56
Sequence 56, Application US/11108528
Publication No. US20050261189A1
GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. Amy
APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
PROLIFERATION
FILE REFERENCE: HYDR-P01-041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-11-108-528-56

Query Match 25.5%; Score 56; DB 7; Length 365;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 NNYCKIKCKLGGVHTACKYGSCLKPNC 26
DB 199 NNLGVKVIKAGVETTCCKCHGVSGSC 224

Publication No. US20060019284A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PatentIn version 3.2
SEQ ID NO 131
LENGTH: 2871
TYPE: PRT
ORGANISM: Homo sapiens
US-11-169-041-131

Query Match 29.8%; Score 65.5; DB 7; Length 2871;
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 14; Conservative 8; Mismatches 13; Indels 21; Gaps 2;

QY 3 YCKIKCKLGGV-----HTACKYGSCLKPNC-----NKVVVSYGLT 37
DB 118 HCNIRCMNGGSCDDHCLCKQGYIGTHCGQVPCSSGCLNGRCVAPNRCACCTYGT 173

RESULT 4
US-10-821-234-916
Sequence 916, Application US/10821234
Publication No. US2005025114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 916
LENGTH: 3002
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-916

Query Match 29.8%; Score 65.5; DB 6; Length 3002;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 14; Conservative 8; Mismatches 13; Indels 21; Gaps 2;

QY 3 YCKIKCKLGGV-----HTACKYGSCLKPNC-----NKVVVSYGLT 37
DB 249 HCNIRCMNGGSCDDHCLCKQGYIGTHCGQVPCSSGCLNGRCVAPNRCACCTYGT 304

RESULT*5
US-11-090-617-706
Sequence 706, Application US/11090617

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 9.67557 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220
Sequence: 1 NNYCKIKLGGVHTACKYGSILKPCNGKNVVSGLTKQ 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

- Database : Published Applications AA New:*
- 1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB pep.*
 - 2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB pep.*
 - 3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB pep.*
 - 4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
 - 5: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB pep.*
 - 6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB pep.*
 - 7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB pep.*
 - 8: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	227	6	US-10-498-026-76
2	168.5	76.6	206	6	US-10-498-026-80
3	65.5	29.8	2871	7	US-11-169-041-131
4	65.5	29.8	3002	6	US-10-821-234-916
5	58	26.4	2911	7	US-11-090-617-706
6	56	25.5	365	7	US-11-108-528-56
7	56	25.5	365	7	US-11-108-528-58
8	55	25.0	271	6	US-10-533-811-1
9	54	24.5	1294	7	US-11-079-463-7534
10	52	23.6	1978	7	US-11-212-443-60
11	51	23.2	298	7	US-11-124-367A-416
12	51	23.2	298	7	US-11-124-367A-417
13	51	23.2	298	7	US-11-124-367A-419
14	51	23.2	313	7	US-11-124-367A-418
15	51	23.2	357	7	US-11-108-528-60
16	51	23.2	359	7	US-11-108-528-62
17	51	23.2	416	7	US-11-124-367A-415
18	50	22.7	1400	6	US-10-821-234-1045
19	49.5	22.5	737	7	US-11-152-366-28
20	49	22.3	271	6	US-10-793-626-2822
21	49	22.3	271	6	US-10-793-626-3308
22	48.5	22.0	245	7	US-11-188-298-8231
23	48.5	22.0	245	7	US-11-188-298-13741
24	48.5	22.0	394	6	US-10-506-454-1398
25	48	21.8	76	6	US-10-467-657-1188

26	48	21.8	292	7	US-11-188-298-5690	Sequence 5690, Ap
27	48	21.8	602	7	US-11-096-568A-30507	Sequence 30507, A
28	48	21.8	701	7	US-11-096-568A-30506	Sequence 30506, A
29	48	21.8	879	7	US-11-096-568A-30505	Sequence 30505, A
30	47.5	21.6	124	5	US-09-995-493-84	Sequence 84, Appl
31	47.5	21.6	683	6	US-10-330-773-346	Sequence 346, App
32	47.5	21.6	702	6	US-10-330-773-341	Sequence 341, App
33	47.5	21.6	892	7	US-11-079-463-9073	Sequence 9073, Ap
34	47.5	21.6	3568	6	US-10-453-372-194	Sequence 194, App
35	47.5	21.6	3570	6	US-10-453-372-178	Sequence 178, App
36	47.5	21.6	3570	6	US-10-453-372-196	Sequence 196, App
37	47.5	21.6	3570	6	US-10-453-372-198	Sequence 198, App
38	47.5	21.6	3570	6	US-10-453-372-200	Sequence 200, App
39	47.5	21.6	3570	6	US-10-453-372-202	Sequence 202, App
40	47.5	21.6	3570	6	US-10-453-372-204	Sequence 204, App
41	47.5	21.6	3570	6	US-10-453-372-206	Sequence 206, App
42	47	21.4	50	7	US-11-172-571-5	Sequence 5, Appl
43	47	21.4	80	7	US-11-172-571-4	Sequence 4, Appl
44	47	21.4	111	7	US-11-188-298-11616	Sequence 11616, A
45	47	21.4	172	7	US-11-096-568A-20968	Sequence 20968, A

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76
Query Match 100.0%; Score 220; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNYCKIKLGGVHTACKYGSILKPCNGKNVVSGLTKQ 39
Db 24 NNYCKIKLGGVHTACKYGSILKPCNGKNVVSGLTKQ 62
RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80
Query Match 76.6%; Score 168.5; DB 6; Length 206;
Best Local Similarity 81.6%; Pred. No. 1.1e-15;
Matches 31; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

; ORGANISM: Vespula vulgaris

US-10-091-135-6

Query Match 100.0%; Score 220; DB 4; Length 46;

Best Local Similarity 100.0%; Pred. No. 3.4e-21;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

RESULT 3

US-10-091-135-93

; Sequence 93, Application US/10091135

; Publication No. US20030039660A1

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; APPLICANT: Spangfort, Michael Dho

; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN

; FILE REFERENCE: 2313/1H587-US1

; CURRENT APPLICATION NUMBER: US/10/091,135

; PRIOR FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: US 60/272,818

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 93

; LENGTH: 50

; TYPE: PRT

; ORGANISM: Vespula vulgaris

US-10-091-135-93

Query Match

Best Local Similarity 100.0%; Score 220; DB 4; Length 50;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

RESULT 4

US-10-091-135-94

; Sequence 94, Application US/10091135

; Publication No. US20030039660A1

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; APPLICANT: Spangfort, Michael Dho

; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN

; FILE REFERENCE: 2313/1H587-US1

; CURRENT APPLICATION NUMBER: US/10/091,135

; PRIOR FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: US 60/272,818

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 94

; LENGTH: 57

; TYPE: PRT

; ORGANISM: Vespula vulgaris

US-10-091-135-94

Query Match

Best Local Similarity 100.0%; Score 220; DB 4; Length 57;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

RESULT 5

US-10-091-135-95

; Sequence 95, Application US/10091135

; Publication No. US20030039660A1

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; APPLICANT: Spangfort, Michael Dho

; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN

; FILE REFERENCE: 2313/1H587-US1

; CURRENT APPLICATION NUMBER: US/10/091,135

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: US 60/272,818

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 95

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Vespula vulgaris

US-10-091-135-95

Query Match

Best Local Similarity 100.0%; Score 220; DB 4; Length 76;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

RESULT 6

US-10-001-245-119

; Sequence 119, Application US/10001245

; Publication No. US20030175312A1

; GENERAL INFORMATION:

; APPLICANT: HOLM, Jens

; APPLICANT: IPSEN, Henrik

; APPLICANT: LARSEN, Jorgen N.

; APPLICANT: SPANGFORT, Michael D.

; TITLE OF INVENTION: No. US20030175312A1el mutant allergens

; FILE REFERENCE: 4305/1H942-US2

; CURRENT APPLICATION NUMBER: US/10/001,245

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/298,170

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/249,361

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 119

; LENGTH: 201

; TYPE: PRT

; ORGANISM: Vespula

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(201)

; OTHER INFORMATION: where X is any amino acid

US-10-001-245-119

Query Match

Best Local Similarity 100.0%; Score 220; DB 4; Length 201;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQ 39

RESULT 7

US-10-001-245-117

; Sequence 117, Application US/10001245

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 59.6908 Seconds
(without alignments)
272.996 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220
Sequence: 1 NNYCKIKLKGCVHTACKYGSILKPNCGNKVVVSYGLTKQ 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	100.0	39	4 US-10-091-135-5	Sequence 5, Appli
2	220	100.0	46	4 US-10-091-135-6	Sequence 6, Appli
3	220	100.0	50	4 US-10-091-135-93	Sequence 93, Appli
4	220	100.0	57	4 US-10-091-135-94	Sequence 94, Appli
5	220	100.0	76	4 US-10-091-135-95	Sequence 95, Appli
6	220	100.0	201	4 US-10-091-135-119	Sequence 119, Appli
7	220	100.0	202	4 US-10-091-245-117	Sequence 117, Appli
8	220	100.0	203	4 US-10-091-245-118	Sequence 118, Appli
9	220	100.0	204	3 US-09-847-208-162	Sequence 162, Appli
10	220	100.0	204	4 US-10-091-135-16	Sequence 16, Appli
11	220	100.0	204	4 US-10-091-135-64	Sequence 64, Appli
12	220	100.0	204	4 US-10-091-135-65	Sequence 65, Appli
13	220	100.0	204	4 US-10-091-135-81	Sequence 81, Appli
14	220	100.0	204	4 US-10-719-553-39	Sequence 39, Appli
15	220	100.0	209	3 US-09-357-806A-22	Sequence 22, Appli
16	220	100.0	210	4 US-10-091-245-214	Sequence 214, Appli
17	220	100.0	227	3 US-09-847-208-170	Sequence 170, Appli
18	220	100.0	227	5 US-10-809-689-82	Sequence 82, Appli
19	216	98.2	204	3 US-09-847-208-166	Sequence 166, Appli
20	216	98.2	204	4 US-10-091-135-66	Sequence 165, Appli
21	214	97.3	204	3 US-09-847-208-165	Sequence 63, Appli
22	214	97.3	204	4 US-10-091-135-63	Sequence 121, Appli
23	212	96.4	198	4 US-10-091-245-121	Sequence 120, Appli
24	205.5	93.4	194	4 US-10-091-245-120	Sequence 163, Appli
25	197	89.5	204	3 US-09-847-208-163	Sequence 67, Appli
26	197	89.5	204	4 US-10-091-135-67	Sequence 4, Appli
27	184	83.6	32	4 US-10-091-135-4	

28	169.5	77.0	205	3	US-09-847-208-167	Sequence 167, Appli
29	169.5	77.0	205	4	US-10-091-135-69	Sequence 69, Appli
30	168.5	76.6	206	3	US-09-847-208-171	Sequence 171, Appli
31	168.5	76.6	206	4	US-10-091-135-68	Sequence 68, Appli
32	168.5	76.6	206	5	US-10-809-689-86	Sequence 86, Appli
33	168	76.4	165	4	US-10-091-245-124	Sequence 124, Appli
34	168	76.4	192	4	US-10-091-245-122	Sequence 122, Appli
35	160	72.7	170	4	US-10-091-245-123	Sequence 123, Appli
36	146	66.4	202	3	US-09-847-208-160	Sequence 160, Appli
37	146	66.4	202	3	US-09-847-208-161	Sequence 161, Appli
38	146	66.4	202	4	US-10-091-135-74	Sequence 74, Appli
39	146	66.4	202	4	US-10-091-135-75	Sequence 75, Appli
40	145	65.9	204	4	US-10-091-135-70	Sequence 70, Appli
41	145	65.9	227	3	US-09-847-208-90	Sequence 90, Appli
42	140	63.6	24	4	US-10-091-135-3	Sequence 3, Appli
43	137	62.3	202	3	US-09-847-208-172	Sequence 172, Appli
44	137	62.3	202	4	US-10-091-135-73	Sequence 73, Appli
45	133.5	60.7	203	3	US-09-847-208-86	Sequence 86, Appli

ALIGNMENTS

RESULT 1
US-10-091-135-5
; Sequence 5, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091-135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Vesputia vulgaris
US-10-091-135-5

Query Match 100.0%; Score 220; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGSILKPNCGNKVVVSYGLTKQ 39
|||||
Db 1 NNYCKIKLKGCVHTACKYGSILKPNCGNKVVVSYGLTKQ 39
|||||

RESULT 2
US-10-091-135-6
; Sequence 6, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091-135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; TYPE: PRT

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKNCVKVWSYGLTKQ 39
-|||||
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKNCVKVWSYGLTKQ 39

RESULT 2
US-08-614-935-2
; Sequence 2, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
US-08-614-935-2

Query Match 100.0%; Score 220; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKNCVKVWSYGLTKQ 39
-|||||
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKNCVKVWSYGLTKQ 39

RESULT 3
US-09-130-287-2
; Sequence 2, Application US/09130287
; Patent No. 6106844
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,287
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
US-09-130-287-2

Query Match 100.0%; Score 220; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKNCVKVWSYGLTKQ 39
-|||||
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKNCVKVWSYGLTKQ 39

RESULT 4
US-09-541-759-6
; Sequence 6, Application US/09541759
; Patent No. 6723322
; GENERAL INFORMATION:
; APPLICANT: Lustigman, Sara
; APPLICANT: Pearlman, Eric
; APPLICANT: Unnasch, Thomas
; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
; FILE REFERENCE: 63475/252
; CURRENT APPLICATION NUMBER: US/09/541,759
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-09-541-759-6

Query Match 100.0%; Score 220; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 11.7595 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220
Sequence: 1 NNYCKIKLGGVHTACKYGLKPNCGNKVVVYGLTKQ 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	204	1	US-08-419-414-9
2	220	100.0	204	1	US-08-614-935-2
3	220	100.0	204	2	US-09-130-287-2
4	220	100.0	204	2	US-09-541-759-6
5	214	97.3	204	1	US-08-614-935-1
6	214	97.3	204	2	US-09-130-287-1
7	180	81.8	31	1	US-08-614-935-46
8	180	81.8	31	2	US-09-130-287-46
9	174	79.1	31	1	US-08-614-935-45
10	174	79.1	31	2	US-09-130-287-45
11	145	65.9	204	1	US-08-614-935-5
12	145	65.9	204	2	US-09-130-287-5
13	133.5	60.7	203	1	US-08-419-414-8
14	133.5	60.7	203	1	US-08-614-935-3
15	133.5	60.7	203	2	US-09-130-287-3
16	132	60.0	205	1	US-08-614-935-4
17	132	60.0	205	2	US-09-130-287-4
18	126	57.3	32	1	US-08-614-935-48
19	126	57.3	32	2	US-09-130-287-48
20	124	56.4	32	1	US-08-614-935-49
21	124	56.4	32	2	US-09-130-287-49
22	119	54.1	32	1	US-08-614-935-42
23	119	54.1	32	2	US-09-130-287-42
24	112.5	51.1	31	1	US-08-614-935-47
25	112.5	51.1	31	2	US-09-130-287-47
26	106	48.2	205	1	US-08-419-414-10
27	106	48.2	205	1	US-08-614-935-6

28	106	48.2	205	1	US-08-614-935-7
29	106	48.2	205	2	US-09-130-287-6
30	106	48.2	205	2	US-09-130-287-7
31	94	42.7	34	1	US-08-614-935-50
32	94	42.7	34	1	US-08-614-935-51
33	94	42.7	34	2	US-09-130-287-50
34	94	42.7	34	2	US-09-130-287-51
35	88.5	40.2	20	1	US-08-614-935-8
36	88.5	40.2	20	2	US-09-130-287-8
37	76.5	34.8	20	1	US-08-614-935-9
38	76.5	34.8	20	2	US-09-130-287-9
39	72.5	33.0	34	1	US-08-614-935-33
40	72.5	33.0	34	2	US-09-130-287-33
41	68	30.9	20	1	US-08-614-935-10
42	68	30.9	20	2	US-09-130-287-10
43	65.5	29.8	1935	2	US-09-949-016-10403
44	65.5	29.8	2871	2	US-09-538-092-1076
45	64	29.1	20	1	US-08-614-935-31

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
; US-08-419-414-9

Query Match 100.0%; Score 220; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 57.6069 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-5

Perfect score: 220

Sequence: 1 NNYCKIKLKGVHTACKYGLKPNCGNKVVSGLTKQ 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	220	100.0	204	1 VAS_VESFL	P35783 vespula fla
2	220	100.0	227	1 VAS_VESVU	Q05110 vespula vul
3	216	98.2	204	1 VAS_VESPE	P35785 vespula pen
4	214	97.3	204	1 VAS_VESMC	P35760 vespula mac
5	197	89.5	204	1 VAS_VESGE	P35784 vespula ger
6	169.5	77.0	205	1 VAS_VESSQ	P35786 vespula squ
7	168.5	76.6	206	1 VAS_VESVI	P35787 vespula vid
8	146	66.4	202	1 VAS1_VESCR	P35781 vespula crabr
9	146	66.4	202	1 VAS2_VESCR	P35782 vespula crabr
10	145	65.9	227	1 VAS2_DOLMA	P10736 dolichovesp
11	137	62.3	202	1 VAS_VESMA	P81657 vespa manda
12	133.5	60.7	203	1 VAS_DOLAR	Q05108 dolichovesp
13	130	59.1	215	1 VAS3_DOLMA	P10737 dolichovesp
14	114	51.8	206	1 VAS_FOLGA	P83377 polistes ga
15	111	50.5	206	1 VAS_FOLDJO	P81656 polistes do
16	111	50.5	227	2 Q68KJB_POLDJO	Q68KJB polistes fu
17	108	49.1	205	1 VAS_POLFUF	P35780 polistes fu
18	106	48.2	205	1 VAS_POLEX	P35759 polistes ex
19	106	48.2	209	1 VAS_POLAN	Q05109 polistes an
20	103	46.8	226	2 Q68KJ9_POLEX	Q68KJ9 polistes ex
21	90.5	41.1	207	1 VAS_POLSR	Q72156 polybia scu
22	67.5	30.7	2884	2 Q4SHN1_TETNG	Q4shn1 tetraodon n
23	65.5	29.8	195	2 Q75N89_HUMAN	Q75N89 homo sapien
24	65.5	29.8	1095	2 Q60784_MOUSE	Q60784 mus musculu
25	65.5	29.8	1365	2 Q75N88_HUMAN	Q75N88 homo sapien
26	65.5	29.8	2871	1 FBNI_BOVIN	P98133 bos taurus
27	65.5	29.8	2871	1 FBNI_HUMAN	P35555 homo sapien
28	65.5	29.8	2871	1 FBNI_MOUSE	Q91554 mus musculu
29	65.5	29.8	2871	1 FBNI_PIG	Q9tv36 sus scrofa
30	65.5	29.8	2871	2 Q75N87_HUMAN	Q75N87 homo sapien
31	65.5	29.8	2872	2 Q9WUH8_RAT	Q9wuh8 rattus norv

Query Match 100.0%; Score 220; DB 1; Length 204;

32	65.5	29.8	3857	2	Q88840_MOUSE	Q88840 mus musculu
33	64.5	29.3	610	2	Q54FR6_DICDI	Q54fr6 dictyosteli
34	63.5	28.9	135	2	Q6S964_PLAFA	Q6s964 plasmodium
35	61	27.7	70	2	Q4SX80_TETNG	Q4sx80 tetraodon n
36	61	27.7	1295	1	GLP1_CAEEL	P13508 caenorhabdi
37	61	27.7	2025	2	Q9SHK4_ARATH	Q9shk4 arabidopsis
38	60.5	27.5	350	2	Q8I3D6_PLAFA7	Q8i3d6 plasmodium
39	60	27.3	396	2	Q8IFU4_GLUOX	Q8fuf4 gluconobact
40	59.5	27.0	311	2	Q5SLJ6_CRYNE	Q5slj6 cryptococcu
41	59.5	27.0	311	2	Q5KD36_CRYNE	Q5kd36 cryptococcu
42	59.5	27.0	315	2	Q55PN7_CRYNE	Q55pn7 cryptococcu
43	59.5	27.0	359	2	Q5KDR9_CRYNE	Q5kdr9 cryptococcu
44	59.5	27.0	542	1	V155_FOWPV	Q9jsa7 fowlpox vir
45	59	26.8	113	2	Q4QQ77_DROME	Q4qq77 drosophila

ALIGNMENTS

RESULT 1

VA5_VESFL

ID VA5_VESFL STANDARD; PRT; 204 AA.

AC P35783;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).

OS Vespula flavopilosa (Yellow jacket) (Wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespula.

OX NCBI_TaxID=30211;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=94044316; PubMed=8227862;

RA Hoffman D.R.;

RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of

antigen 5 molecules and the structural basis of antigenic cross-

reactivity.";

RL J. Allergy Clin. Immunol. 92:707-716(1993).

CC -!- FUNCTION: May have an ancestral function in the promotion of ovum

CC fertilization by sperm.

CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.

CC -!- ALLERGEN: Causes an allergic reaction in human.

CC -!- SIMILARITY: Belongs to the CRISP family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC PIR; A44583; A44583.

CC HSSP; Q05110; 1QNK.

CC SMR; P35783; 1-204.

CC InterPro; IPR001283; Allrgn_V5/TpXl.

CC InterPro; IPR002413; V5_allergen.

CC Pfam; PF00188; SCP; 1.

CC PRINTS; PR00838; V5ALLERGEN.

CC PRINTS; PR00837; V5TPXLLIKE.

CC ProDom; PD000542; Allrgn_V5/TpXl; 1.

CC SMART; SM00198; SCP; 1.

CC PROSITE; PS01009; CRISP_1; 1.

CC PROSITE; PS01010; CRISP_2; 1.

CC Allergen; Direct protein sequencing.

FT DISULFID 4 17 By similarity.

FT DISULFID 8 101 By similarity.

FT DISULFID 26 94 By similarity.

FT DISULFID 170 187 By similarity.

FT SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;


```
RESULT 3
B37329
antigen 5 - eastern yellowjacket
C;Species: Vespula maculifrons (eastern yellowjacket)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: B37329
R;Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A;Reference number: A37329
A;Accession: B37329
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35760; UNIPARC:UPI00000138092
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 97.3%; Score 214; DB 2; Length 204;
Best Local Similarity 97.4%; Pred. No. 1.8e-19;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGSCLKPNCNGKVVVSYGLTKQ 39
DB 1 NNYCKIKCLKGGVHTACKYGSCLKPNCNGKVVVSYGLTKQ 39

RESULT 4
B44583
venom allergen antigen Ves g 5 - German yellowjacket
C;Species: Vespula germanica (German yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: B44583; A44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: B44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35784; UNIPARC:UPI00000138090
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 89.5%; Score 197; DB 2; Length 204;
Best Local Similarity 89.7%; Pred. No. 2.5e-17;
Matches 35; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGSCLKPNCNGKVVVSYGLTKQ 39
DB 1 NNYCKIKCLKGGVHTACKYGSCLKPNCANKKVVAYGLTKQ 39

RESULT 5
D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C;Species: Vespula squamosa (southern yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: D44583; D44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: D44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-205 <HOF>
A;Cross-references: UNIPROT:P35786; UNIPARC:UPI00000138094
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 77.0%; Score 169.5; DB 2; Length 205;
Best Local Similarity 81.6%; Pred. No. 6.8e-14;
Matches 31; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 NYCKIKCLKGGVHTACKYGSCLKPNCNGKVVVSYGLTK 38
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DB 2 DYCKIKCLKGGVHTACKYGTSTKPNCGKNVVKSYGVTO 39

RESULT 6
E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C;Species: Vespula vidua
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: E44583; E44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: E44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-206 <HOF>
A;Cross-references: UNIPROT:P35787; UNIPARC:UPI00000138095
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 76.6%; Score 168.5; DB 2; Length 206;
Best Local Similarity 81.6%; Pred. No. 9.1e-14;
Matches 31; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 NYCKIKCLKGGVHTACKYGSCLKPNCNGKVVVSYGLTK 38
DB 3 NYCKIKCLKGGVHTACKYGTSTKPNCGKNVVKAYGLTE 40

RESULT 7
H44583
venom allergen antigen Vesp c 5.02 - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: H44583; H44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: H44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-202 <HOF>
A;Cross-references: UNIPROT:P35782; UNIPARC:UPI00000138080
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 66.4%; Score 146; DB 2; Length 202;
Best Local Similarity 70.0%; Pred. No. 5.8e-11;
Matches 28; Conservative 3; Mismatches 7; Indels 2; Gaps 2;

QY 1 NNYCKIKCLKGGVHTACKYGSCLKPNCNGKVVVSYGLTKQ 39
DB 1 NNYCKIKC-RSGIHTLCKYGTSTKPNCGKNVVKASGLTKQ 39

RESULT 8
G44583
venom allergen antigen Vesp c 5.01 - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: G44583; G44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: G44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-202 <HOF>
A;Cross-references: UNIPROT:P35781; UNIPARC:UPI0000013807C
C;Superfamily: yellowjacket venom allergen antigen 5
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 8.18702 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-5

Perfect score: 220

Sequence: 1 NNYCKIKCLKGGVHTACKYGLKPKNCNKKVVSYGLTKQ 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	100.0	204	2 A44583	venom allergen ant
2	216	98.2	204	2 C44583	venom allergen ant
3	214	97.3	204	2 B37329	antigen 5 - easter
4	197	89.5	204	2 B44583	venom allergen ant
5	169.5	77.0	205	2 D44583	venom allergen ant
6	168.5	76.6	206	2 E44583	venom allergen ant
7	146	66.4	202	2 H44583	venom allergen ant
8	146	66.4	202	2 G44583	venom allergen ant
9	145	65.9	227	2 A31085	antigen 5-2 precu
10	132	60.0	213	2 B31085	antigen 5-3 precu
11	108	49.1	205	2 F44583	venom allergen ant
12	106	48.2	205	2 A37329	antigen 5 - paper
13	65.5	29.8	2871	2 A5567	fibrillin I - bovi
14	65.5	29.8	2871	2 A5567	fibrillin-1 precu
15	65.5	29.8	3002	2 A47221	fibrillin-1 precu
16	61	27.7	1295	2 A32901	glp1 protein precu
17	61	27.7	2025	2 D86201	protein F12K11.6 [
18	58.5	26.6	258	2 A33953	enterotoxin D prec
19	58.5	26.6	401	2 G96972	hypothetical prote
20	58.5	26.6	1469	2 T19459	hypothetical prote
21	58.5	26.6	2907	2 A57278	fibrillin-2 precu
22	58	26.4	1712	2 A38261	masking protein pr
23	58	26.4	2918	2 A54105	fibrillin-2 precu
24	56.5	25.7	292	2 H81857	hypothetical prote
25	56.5	25.7	342	2 B81086	hypothetical prote
26	56	25.5	2496	2 A71616	secreted protein P
27	54	24.5	211	2 B58853	venom allergen Sol
28	54	24.5	212	2 B37330	venom allergen tii
29	54	24.5	251	2 A55035	cysteine-rich prot

30	53	24.1	362	2 I40304	outer membrane lip
31	53	24.1	453	1 A25326	acid phosphatase (
32	53	24.1	4910	2 B64942	probable membrane
33	52.5	23.9	730	2 B85013	hypothetical prote
34	52.5	23.9	730	2 T10539	hypothetical prote
35	52	23.6	79	2 T07917	antifungal protein
36	52	23.6	79	2 T10243	antifungal protein
37	52	23.6	87	2 T00564	gibberellin-regula
38	52	23.6	95	2 H72271	ferredoxin - Therm
39	52	23.6	143	2 C97970	hypothetical prote
40	52	23.6	1975	2 B81192	hemagglutinin/hemo
41	52	23.6	1995	2 G81044	hemagglutinin/hemo
42	51.5	23.4	341	2 T05764	hypothetical prote
43	51.5	23.4	1294	2 S77690	probable membrane
44	51	23.2	80	2 T10183	antifungal protein
45	50.5	23.0	260	2 B89969	enterotoxin Seo [1

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol.
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>

A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5
Query Match 100.0%; Score 220; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKCLKGGVHTACKYGLKPKNCNKKVVSYGLTKQ 39
Db 1 NNYCKIKCLKGGVHTACKYGLKPKNCNKKVVSYGLTKQ 39

RESULT 2

C44583
venom allergen antigen Ves p 5 - western yellowjacket
C:Species: Vespula pensylvanica (western yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: C44583; C44522
R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol.
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: C44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>

A:Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C:Superfamily: yellowjacket venom allergen antigen 5
Query Match 98.2%; Score 216; DB 2; Length 204;
Best Local Similarity 94.9%; Pred. No. 1e-19;
Matches 37; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKCLKGGVHTACKYGLKPKNCNKKVVSYGLTKQ 39
Db 1 NNYCKIKCLKGGVHTACKYGLKPKNCNKKVVSYGLTKE 39

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XX SQ Sequence 39 AA;
Query Match 100.0%; Score 220; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVWVSGLTKQ 39
|||||
Db 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVWVSGLTKQ 39

RESULT 2
AAE28812
ID AAE28812 standard; peptide; 46 AA.
XX
AC AAE28812;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #6.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
DR N-PSDB; AAD46230.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 151; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 46 AA;
Query Match 100.0%; Score 220; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVWVSGLTKQ 39
|||||
Db 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVWVSGLTKQ 39

RESULT 3
AAE28827
ID AAE28827 standard; peptide; 50 AA.
XX
AC AAE28827;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #14.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
DR N-PSDB; AAD46272.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 50 AA;
Query Match 100.0%; Score 220; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVWVSGLTKQ 39
|||||
Db 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVWVSGLTKQ 39

RESULT 4
AAE28828
ID AAE28828 standard; peptide; 57 AA.
XX
AC AAE28828;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #15.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 54.3321 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220

Sequence: 1 NNYCKIKLGKGVHTACKYKSLKPCNKGVVSYGLTKQ 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	39	Aae28811	Aae28811 Vesputa v
2	220	100.0	46	Aae28812	Aae28812 Vesputa v
3	220	100.0	50	Aae28827	Aae28827 Vesputa v
4	220	100.0	57	Aae28828	Aae28828 Vesputa v
5	220	100.0	76	Aae28829	Aae28829 Vesputa v
6	220	100.0	204	Aaw35688	Aaw35688 Vespid an
7	220	100.0	204	Aay45217	Aay45217 Wild type
8	220	100.0	204	Abg66983	Abg66983 Wasp veno
9	220	100.0	204	Abg67052	Abg67052 Wasp veno
10	220	100.0	204	Abg67104	Abg67104 Wasp veno
11	220	100.0	204	Abg67103	Abg67103 Wasp veno
12	220	100.0	204	Aae28820	Aae28820 Vesputa v
13	220	100.0	209	Abm00031	Abm00031 Allergen
14	220	100.0	227	Aay25644	Aay25644 Vesputa s
15	220	100.0	227	Aae13071	Aae13071 Vesputa v
16	220	100.0	227	Adc34893	Adc34893 Wasp alle
17	214	97.3	204	Aaw35687	Aaw35687 Vespid an
18	214	97.3	204	Abg66977	Abg66977 Wasp veno
19	184	83.6	32	Aae28810	Aae28810 Vesputa v
20	180	81.8	31	Aaw35648	Aaw35648 T cell pe
21	174	79.1	31	Aaw35647	Aaw35647 T cell pe
22	168.5	76.6	206	Aay25648	Aay25648 Vesputa s
23	168.5	76.6	206	Adc34897	Adc34897 Wasp alle
24	145	65.9	204	Aaw35691	Aaw35691 Vespid an

25	140	63.6	24	5	AAE28809	Aae28809 Vesputa v
26	133.5	60.7	203	2	AAW35689	Aaw35689 Vespid an
27	132	60.0	205	2	AAW35690	Aaw35690 Vespid an
28	126	57.3	32	2	AAW35650	Aaw35650 T cell pe
29	124	56.4	32	2	AAW35651	Aaw35651 T cell pe
30	119	54.1	32	2	AAW35644	Aaw35644 Immunomod
31	112.5	51.1	31	2	AAW35649	Aaw35649 T cell pe
32	107	48.6	18	5	AAE28808	Aae28808 Vesputa v
33	106	48.2	205	2	AAW35693	Aaw35693 Vespid an
34	106	48.2	205	2	AAW35692	Aaw35692 Vespid an
35	106	48.2	205	5	AAE28821	Aae28821 Polistes
36	94	42.7	34	2	AAW35652	Aaw35652 T cell pe
37	94	42.7	34	2	AAW35653	Aaw35653 T cell pe
38	88.5	40.2	20	2	AAW35619	Aaw35619 Immunomod
39	79.5	36.1	34	2	AAW35635	Aaw35635 Immunomod
40	76.5	34.8	20	2	AAW35620	Aaw35620 Immunomod
41	71	32.3	20	2	AAW35633	Aaw35633 Immunomod
42	68	30.9	20	2	AAW35694	Aaw35694 D. macula
43	65.5	29.8	2871	8	ABM81619	Abm81619 Tumour-as
44	65.5	29.8	2871	9	ADX05916	Adx05916 Cyclin-de
45	65.5	29.8	2871	9	ADZ70705	Adz70705 Human pro

ALIGNMENTS

RESULT 1
AAE28811
ID AAE28811 standard; peptide; 39 AA.
XX
AC AAE28811;
XX
DT 27-DEC-2002 (first entry)
XX

DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #5.

XX Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX

OS Vesputa vulgaris.

XX WO200270665-A2.

XX 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US006765.

XX 02-MAR-2001; 2001US-0272818P.

XX (UYRQ) UNIV ROCKEFELLER.
(ALKA-) ALK-ABELLO AS.

XX King TP, Spangfort MD;

XX WPI; 2002-698751/75.

XX N-PSDB; AAD46229.

XX New allergen hybrid protein having reduced allergenicity but retaining immunogenicity, useful for treating allergy or immune system related diseases.

XX Claim 17; Page 151; 222pp; English.

XX The present invention relates to recombinant allergen hybrid proteins having reduced allergenicity but retaining immunogenicity. The hybrid proteins comprise a peptide epitope sequence of an allergen protein and a scaffold protein that is structurally homologous to the allergen protein. Sequences of the invention comprise a native conformation and the peptide epitope sequence is present in a surface accessible region of the hybrid protein corresponding to its position in the allergen protein. The hybrid proteins are useful for treating allergy or immune system related diseases. They are also used as vaccines. The present sequence is Vesputa vulgaris antigen 5 (Ves V5) allergen peptide